

SEQUENCE LISTING

<110> Lanahan, Mike

<120> Self-processing Plants and Plant Parts

<130> 109846.317

<140> US 60/315,281

<141> 2001-08-27

<160> 112

<170> FastSEQ for Windows Version 4.0

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 Ala Lys Asp Arg Phe Ile Glu Ile Lys Asp Gly Lys Ala Glu Val Trp
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 Ile Leu Gln Gly Val Glu Glu Ile Phe Tyr Glu Lys Pro Asp Thr Ser
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 85 90 95
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 Pro Thr Asp Ile Asp Val Thr Asn Tyr Val Arg Ile Val Leu Ser Glu
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 Gly Pro Lys Ile Glu Gly Tyr Glu Asp Ala Ile Ile Tyr Glu Ile His
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cgcatgtca	tgagcgccga	ggagaagttc	ccaggcaagg	tgcgcgcgtg	ggtcaagtgc	1380
aacgcggcgc	tggcgacca	catcatggcc	ggcgcgcgac	tgctcgccgt	caccagccgc	1440
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gcgtccaccg	gtggactcgt	cgacaccatc	atcgaaggca	agaccgggtt	ccacatgggc	1560
cgctcagcg	tcgactgcaa	cgtcgtggag	ccggcggaag	tcaagaaggt	ggccaccacc	1620
ttgcagcgcg	ccatcaaggt	ggtcggcacg	ccggcgtagc	aggagatggt	gaggaactgc	1680
atgatccagg	atctctcctg	gaagggccct	gccaaagaact	gggagaacgt	gctgctcagc	1740
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gagaacgtgg	ccgcgccc					1818

<210> 8

<211> 606

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic


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<400> 8
Met Ala Ala Leu Ala Thr Ser Gln Leu Val Ala Thr Arg Ala Gly Leu
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Gly Val Pro Asp Ala Ser Thr Phe Arg Arg Gly Ala Ala Gln Gly Leu
 20          25          30
Arg Gly Ala Arg Ala Ser Ala Ala Asp Thr Leu Ser Met Arg Thr
 35          40          45
Ser Ala Arg Ala Ala Pro Arg His Gln His Gln Gln Ala Arg Arg Gly
 50          55          60
Ala Arg Phe Pro Ser Leu Val Val Cys Ala Ser Ala Gly Met Asn Val
 65          70          75          80
Val Phe Val Gly Ala Glu Met Ala Pro Trp Ser Lys Thr Gly Gly Leu
 85          90          95
Gly Asp Val Leu Gly Gly Leu Pro Pro Ala Met Ala Ala Asn Gly His
100          105          110
Arg Val Met Val Val Ser Pro Arg Tyr Asp Gln Tyr Lys Asp Ala Trp
115          120          125
Asp Thr Ser Val Val Ser Glu Ile Lys Met Gly Asp Gly Tyr Glu Thr
130          135          140
Val Arg Phe Phe His Cys Tyr Lys Arg Gly Val Asp Arg Val Phe Val
145          150          155          160
Asp His Pro Leu Phe Leu Glu Arg Val Trp Gly Lys Thr Glu Glu Lys
165          170          175
Ile Tyr Gly Pro Val Ala Gly Thr Asp Tyr Arg Asp Asn Gln Leu Arg
180          185          190
Phe Ser Leu Leu Cys Gln Ala Ala Leu Glu Ala Pro Arg Ile Leu Ser
195          200          205
Leu Asn Asn Asn Pro Tyr Phe Ser Gly Pro Tyr Gly Glu Asp Val Val
210          215          220
Phe Val Cys Asn Asp Trp His Thr Gly Pro Leu Ser Cys Tyr Leu Lys
225          230          235          240
Ser Asn Tyr Gln Ser His Gly Ile Tyr Arg Asp Ala Lys Thr Ala Phe
245          250          255
Cys Ile His Asn Ile Ser Tyr Gln Gly Arg Phe Ala Phe Ser Asp Tyr
260          265          270
Pro Glu Leu Asn Leu Pro Glu Arg Phe Lys Ser Ser Phe Asp Phe Ile
275          280          285
Asp Gly Tyr Glu Lys Pro Val Glu Gly Arg Lys Ile Asn Trp Met Lys
290          295          300
Ala Gly Ile Leu Glu Ala Asp Arg Val Leu Thr Val Ser Pro Tyr Tyr
305          310          315          320
Ala Glu Glu Leu Ile Ser Gly Ile Ala Arg Gly Cys Glu Leu Asp Asn
325          330          335
Ile Met Arg Leu Thr Gly Ile Thr Gly Ile Val Asn Gly Met Asp Val
340          345          350
Ser Glu Trp Asp Pro Ser Arg Asp Lys Tyr Ile Ala Val Lys Tyr Asp
355          360          365
Val Ser Thr Ala Val Glu Ala Lys Ala Leu Asn Lys Glu Ala Leu Gln
370          375          380
Ala Glu Val Gly Leu Pro Val Asp Arg Asn Ile Pro Leu Val Ala Phe
385          390          395          400
Ile Gly Arg Leu Glu Glu Gln Lys Gly Pro Asp Val Met Ala Ala Ala
405          410          415
Ile Pro Gln Leu Met Glu Met Val Glu Asp Val Gln Ile Val Leu Leu
420          425          430
Gly Thr Gly Lys Lys Lys Phe Glu Arg Met Leu Met Ser Ala Glu Glu
435          440          445
Lys Phe Pro Gly Lys Val Arg Ala Val Val Lys Phe Asn Ala Ala Leu

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450	Ala His His Ile Met	455	Ala Gly Ala Asp Val	460	Ala Val Thr Ser Arg
465	Phe Glu Pro Cys Gly	470	Leu Ile Gln Leu Gln	475	Met Arg Tyr Gly Thr
	485		490		495
	Pro Cys Ala Cys Ala		Ser Thr Gly Gly Leu		Val Asp Thr Ile Ile Glu
	500		505		510
	Gly Lys Thr Gly Phe		His Met Gly Arg Leu		Ser Val Asp Cys Asn Val
	515		520		525
	Val Glu Pro Ala Asp		Val Lys Lys Val Ala		Thr Thr Leu Gln Arg Ala
	530		535		540
	Ile Lys Val Val Gly		Thr Pro Ala Tyr Glu		Glu Met Val Arg Asn Cys
	545		550		555
	Met Ile Gln Asp Leu		Ser Trp Lys Gly Pro		Ala Lys Asn Trp Glu Asn
	565		570		575
	Val Leu Leu Ser Leu		Gly Val Ala Gly Gly		Glu Pro Gly Val Glu Gly
	580		585		590
	Glu Glu Ile Ala Pro		Leu Ala Lys Glu Asn		Val Ala Ala Pro
	595		600		605

<210> 9
 <211> 2223
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 9
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 gccggcatct ccgcgatctg gataccgccca gcttccaagg gcatgtccgg gggctactcg 180
 atgggctacg acccgctacga ctacttcgac ctccggcgagt actaccagaa gggcacgggtg 240
 gagacgcgct tcgggtccaa gcaggagctc atcaacatga tcaacacggc gcacgcctac 300
 ggcatcaagg tcatcgcgga catcgtgatc aaccacaggg ccggcgggcga cctggagtg 360
 aaccggttcg tcggcgacta caccctggacg gacttctcca aggtcgctc cggcaagtac 420
 accgccaact acctcgactt ccaccccaac gagctgcacg cgggcgactc cggcacgttc 480
 ggcggtctacc cggacatctg ccacgacaag tcctgggacc agtactggct ctgggcctcg 540
 caggagtctt acgcggccta cctgcgctcc atcggcatcg acgcgtggcg cttcgactac 600
 gtcaagggtc acggggcctg ggtggtcaa gactggctca actgggtggg cggctggcg 660
 gtgggcgagt actgggacac caacgtcgac gcgctgctca actgggccta ctctccggc 720
 gccaaaggtg tcgacttccc cctgtactac aagatggacg cggccttcga caacaagaac 780
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 aaggccgtga ccttcgtcgc caaccacgac acggacatca tctggaacaa gtaccggcg 900
 tacgccttca tcctcaccta cgagggccag cccacgatct tctaccgga ctacgaggag 960
 tggctgaaca aggacaagct caagaacctg atctggattc acgacaacct cgcgggcggc 1020
 tccactagta tcgtgtacta cgactccgac gagatgatct tcgtccgcaa cggctacggc 1080
 tccaagccc gctgatcac gtacatcaac ctgggtcctt ccaaggtggg ccgctgggtg 1140
 tacgtcccga agttcgccgg cgcgtgcac caccagtaga ccggcaacct cggcggtgg 1200
 gtggacaagt acgtgtactc ctccggtgg gtctacctgg aggcccggc ctacgacccc 1260
 gccaacggcc agtacggcta ctccgtgtgg tcctactgcg gcgtcggcac atcgattgct 1320
 ggcacctctg aggccgacag ggtcctcacc gtcagcccct actacgccga ggagctcatc 1380
 tccggcatcg ccaggggctg cgagctcgac aacatcatgc gcctcaccgg catcaccggc 1440
 atcgtcaacg gcatggacgt cagcaggtgg gaccccagca gggacaagta catcgccgtg 1500
 aagtacgacg tgtcgacggc cgtggaggcc aaggcgctga acaaggaggc gctgcaggcg 1560
 gaggtcgggc tcccggtgga ccggaacatc ccgctggtgg cgttcacggc caggctggaa 1620
 gagcagaagg gccccgacgt catggcggcc gccatcccgc agctcatgga gatggtggag 1680

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gacgtgcaga tcgttctgct gggcacgggc aagaagaagt tcgagcgcat gctcatgagc 1740
gccgaggaga agttcccagg caaggtgcgc gccgtggtca agttcaacgc ggcgctggcg 1800
caccacatca tggccggcgc cgacgtgctc gccgtcacca gccgcttcga gccctgcggc 1860
ctcatccagc tgcaggggat gcgatacgga acgccctgcg cctgcgcgctc caccggtgga 1920
ctcgtcgaca ccatcatcga aggcaagacc gggttccaca tgggcccgcct cagcgtcgac 1980
tgcaacgtcg tggagccggc ggacgtcaag aaggtggcca ccaccttgca gcgcgccatc 2040
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tcctggaagg gccctgccaa gaactgggag aacgtgctgc tcagcctcgg ggtcgccggc 2160
ggcgagccag gggttgaagg cgaggagatc gcgccgctcg ccaaggagaa cgtggccgcg 2220
ccc

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<210> 10
 <211> 741
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 10

Met	Ala	Lys	Tyr	Leu	Glu	Leu	Glu	Glu	Gly	Gly	Val	Ile	Met	Gln	Ala
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Phe	Tyr	Trp	Asp	Val	Pro	Ser	Gly	Gly	Ile	Trp	Trp	Asp	Thr	Ile	Arg
			20					25					30		
Gln	Lys	Ile	Pro	Glu	Trp	Tyr	Asp	Ala	Gly	Ile	Ser	Ala	Ile	Trp	Ile
		35					40					45			
Pro	Pro	Ala	Ser	Lys	Gly	Met	Ser	Gly	Gly	Tyr	Ser	Met	Gly	Tyr	Asp
	50					55					60				
Pro	Tyr	Asp	Tyr	Phe	Asp	Leu	Gly	Glu	Tyr	Tyr	Gln	Lys	Gly	Thr	Val
65				70					75					80	
Glu	Thr	Arg	Phe	Gly	Ser	Lys	Gln	Glu	Leu	Ile	Asn	Met	Ile	Asn	Thr
			85					90					95		
Ala	His	Ala	Tyr	Gly	Ile	Lys	Val	Ile	Ala	Asp	Ile	Val	Ile	Asn	His
		100					105					110			
Arg	Ala	Gly	Gly	Asp	Leu	Glu	Trp	Asn	Pro	Phe	Val	Gly	Asp	Tyr	Thr
	115						120					125			
Trp	Thr	Asp	Phe	Ser	Lys	Val	Ala	Ser	Gly	Lys	Tyr	Thr	Ala	Asn	Tyr
	130					135					140				
Leu	Asp	Phe	His	Pro	Asn	Glu	Leu	His	Ala	Gly	Asp	Ser	Gly	Thr	Phe
145				150					155					160	
Gly	Gly	Tyr	Pro	Asp	Ile	Cys	His	Asp	Lys	Ser	Trp	Asp	Gln	Tyr	Trp
			165					170					175		
Leu	Trp	Ala	Ser	Gln	Glu	Ser	Tyr	Ala	Ala	Tyr	Leu	Arg	Ser	Ile	Gly
		180					185					190			
Ile	Asp	Ala	Trp	Arg	Phe	Asp	Tyr	Val	Lys	Gly	Tyr	Gly	Ala	Trp	Val
	195					200						205			
Val	Lys	Asp	Trp	Leu	Asn	Trp	Trp	Gly	Gly	Trp	Ala	Val	Gly	Glu	Tyr
	210				215						220				
Trp	Asp	Thr	Asn	Val	Asp	Ala	Leu	Leu	Asn	Trp	Ala	Tyr	Ser	Ser	Gly
225				230					235					240	
Ala	Lys	Val	Phe	Asp	Phe	Pro	Leu	Tyr	Tyr	Lys	Met	Asp	Ala	Ala	Phe
			245					250					255		
Asp	Asn	Lys	Asn	Ile	Pro	Ala	Leu	Val	Glu	Ala	Leu	Lys	Asn	Gly	Gly
		260					265					270			
Thr	Val	Val	Ser	Arg	Asp	Pro	Phe	Lys	Ala	Val	Thr	Phe	Val	Ala	Asn
	275					280						285			
His	Asp	Thr	Asp	Ile	Ile	Trp	Asn	Lys	Tyr	Pro	Ala	Tyr	Ala	Phe	Ile
	290					295					300				

Leu Thr Tyr Glu Gly Gln Pro Thr Ile Phe Tyr Arg Asp Tyr Glu Glu
 305 310 315 320
 Trp Leu Asn Lys Asp Lys Leu Lys Asn Leu Ile Trp Ile His Asp Asn
 325 330 335
 Leu Ala Gly Gly Ser Thr Ser Ile Val Tyr Tyr Asp Ser Asp Glu Met
 340 345 350
 Ile Phe Val Arg Asn Gly Tyr Gly Ser Lys Pro Gly Leu Ile Thr Tyr
 355 360 365
 Ile Asn Leu Gly Ser Ser Lys Val Gly Arg Trp Val Tyr Val Pro Lys
 370 375 380
 Phe Ala Gly Ala Cys Ile His Glu Tyr Thr Gly Asn Leu Gly Gly Trp
 385 390 395 400
 Val Asp Lys Tyr Val Tyr Ser Ser Gly Trp Val Tyr Leu Glu Ala Pro
 405 410 415
 Ala Tyr Asp Pro Ala Asn Gly Gln Tyr Gly Tyr Ser Val Trp Ser Tyr
 420 425 430
 Cys Gly Val Gly Thr Ser Ile Ala Gly Ile Leu Glu Ala Asp Arg Val
 435 440 445
 Leu Thr Val Ser Pro Tyr Tyr Ala Glu Glu Leu Ile Ser Gly Ile Ala
 450 455 460
 Arg Gly Cys Glu Leu Asp Asn Ile Met Arg Leu Thr Gly Ile Thr Gly
 465 470 475 480
 Ile Val Asn Gly Met Asp Val Ser Glu Trp Asp Pro Ser Arg Asp Lys
 485 490 495
 Tyr Ile Ala Val Lys Tyr Asp Val Ser Thr Ala Val Glu Ala Lys Ala
 500 505 510
 Leu Asn Lys Glu Ala Leu Gln Ala Glu Val Gly Leu Pro Val Asp Arg
 515 520 525
 Asn Ile Pro Leu Val Ala Phe Ile Gly Arg Leu Glu Gln Lys Gly
 530 535 540
 Pro Asp Val Met Ala Ala Ala Ile Pro Gln Leu Met Glu Met Val Glu
 545 550 555 560
 Asp Val Gln Ile Val Leu Leu Gly Thr Gly Lys Lys Lys Phe Glu Arg
 565 570 575
 Met Leu Met Ser Ala Glu Glu Lys Phe Pro Gly Lys Val Arg Ala Val
 580 585 590
 Val Lys Phe Asn Ala Ala Leu Ala His His Ile Met Ala Gly Ala Asp
 595 600 605
 Val Leu Ala Val Thr Ser Arg Phe Glu Pro Cys Gly Leu Ile Gln Leu
 610 615 620
 Gln Gly Met Arg Tyr Gly Thr Pro Cys Ala Cys Ala Ser Thr Gly Gly
 625 630 635 640
 Leu Val Asp Thr Ile Ile Glu Gly Lys Thr Gly Phe His Met Gly Arg
 645 650 655
 Leu Ser Val Asp Cys Asn Val Val Glu Pro Ala Asp Val Lys Lys Val
 660 665 670
 Ala Thr Thr Leu Gln Arg Ala Ile Lys Val Val Gly Thr Pro Ala Tyr
 675 680 685
 Glu Glu Met Val Arg Asn Cys Met Ile Gln Asp Leu Ser Trp Lys Gly
 690 695 700
 Pro Ala Lys Asn Trp Glu Asn Val Leu Leu Ser Leu Gly Val Ala Gly
 705 710 715 720
 Gly Glu Pro Gly Val Glu Gly Glu Glu Ile Ala Pro Leu Ala Lys Glu
 725 730 735
 Asn Val Ala Ala Pro
 740

<210> 11
 <211> 1515
 <212> DNA
 <213> Zea mays

<400> 11
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 ctttgttact tcatcatgca tgaacatttg tggaaactac tagcttacaa gcattagtga 120
 cagctcagaa aaaagtattc tatgaaagggt ttcatgtgta ccgtgggaaa tgagaaatgt 180
 tgccaactca aacaccttca atatgttggt tgcaggcaaa ctcttctgga agaaagggtgt 240
 ctaaaactat gaacgggtta cagaaaggta taaaccacgg ctgtgcattt tggaagtatc 300
 atctatagat gtctgttgag gggaaagccg tacgccaacg ttattttactc agaaacagct 360
 tcaacacaca gttgtctgct ttatgatggc atctccaccc aggcacccac catcacctat 420
 ctctcgtgcc tgtttatttt cttgcccctt ctgatcataa aaaaacatta agagtttgca 480
 aacatgcata ggcatatcaa tatgctcatt tattaatttg ctacgagatc atcttcctac 540
 tctttacttt atttattggt tgaaaaatat gtctgcacc tagggagctc gtatacagta 600
 ccaatgcac ttcatataat gtgaatttca gaaaggaagt aggaacctat gagagtattt 660
 ttcaaaatta attagcggct tctattatgt ttatagcaaa ggccaagggc aaaattggaa 720
 cactaatgat ggttgggttg atgagtcctgt cgattacttg caagaaatgt gaacctttgt 780
 ttctgtgcgt gggcataaaa caaacagctt ctagcctctt ttacggtact tgcacttgca 840
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 ttcatgggtt ttgatgtctt tacacagttc atctccacca gtatgccctc ctcatactct 960
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 ttctgatctc gcagccacct ttttttgttc tgttgtaagt ataccttccc ttaccatctt 1080
 tatctgttag tttaatttgt aattgggaag tattagtgga aagaggatga gatgctatca 1140
 tctatgtact ctgcaaatgc atctgacgtt atatgggctg ctcatataa tttgaattgc 1200
 tccattcttg ccgacaatat attgcaagggt atatgcctag ttccatcaaa agttctgttt 1260
 ttctattcta aaagcatttt agtggcacac aatttttgtc catgagggaa aggaaatctg 1320
 ttttggttac tttgcttgag gtgcattctt catatgtcca gttttatgga agtaataaac 1380
 ttcagtttgg tcataagatg tcatattaaa gggcaaacat atattcaatg ttcaattcat 1440
 cgtaaatgtt cccttttgtt aaaagattgc atactcattt atttgagttg caggtgtatc 1500
 tagtagttgg aggag 1515

<210> 12
 <211> 673
 <212> DNA
 <213> Zea mays

<400> 12
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 ttggcatgta aagctccaag aatttgttgt atccttaaca actcacagaa catcaaccaa 120
 aattgcacgt caagggtatt gggtaagaaa caatcaaaca aatcctctct gtgtgcaaag 180
 aaacacgggtg agtcatgccg agatcatact catctgatat acatgcttac agctcacaag 240
 acattacaaa caactcatat tgcattacaa agatcgtttc atgaaaaata aaataggccg 300
 gacaggacaa aaatccttga cgtgtaaaagt aaattttaca caaaaaaaaaa gccatatgtc 360
 aagctaaatc taattcgttt tacgtagatc aacaacctgt agaaggcaac aaaactgagc 420
 cacgcagaag tacagaatga ttccagatga accatcgacg tgctacgtaa agagagtgc 480
 gagtcatata catttggcaa gaaaccatga agctgcctac agccgtctcg gtggcataag 540
 aacacaagaa attgtgttaa ttaatcaaag ctataaataa cgctcgcatg cctgtgcact 600
 tctccatcac caccactggg tcttcagacc attagcttta tctactccag agcgcagaag 660
 aacccgatcg aca 673

<210> 13
 <211> 454
 <212> PRT
 <213> Artificial Sequence

<220>

<223> synthetic

<400> 13

Met Arg Val Leu Leu Val Ala Leu Ala Leu Leu Ala Leu Ala Ala Ser
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 Ala Thr Ser Ala Lys Tyr Leu Glu Leu Glu Glu Gly Gly Val Ile Met
 20 25 30
 Gln Ala Phe Tyr Trp Asp Val Pro Ser Gly Gly Ile Trp Trp Asp Thr
 35 40 45
 Ile Arg Gln Lys Ile Pro Glu Trp Tyr Asp Ala Gly Ile Ser Ala Ile
 50 55 60
 Trp Ile Pro Pro Ala Ser Lys Gly Met Ser Gly Gly Tyr Ser Met Gly
 65 70 75 80
 Tyr Asp Pro Tyr Asp Tyr Phe Asp Leu Gly Glu Tyr Tyr Gln Lys Gly
 85 90 95
 Thr Val Glu Thr Arg Phe Gly Ser Lys Gln Glu Leu Ile Asn Met Ile
 100 105 110
 Asn Thr Ala His Ala Tyr Gly Ile Lys Val Ile Ala Asp Ile Val Ile
 115 120 125
 Asn His Arg Ala Gly Gly Asp Leu Glu Trp Asn Pro Phe Val Gly Asp
 130 135 140
 Tyr Thr Trp Thr Asp Phe Ser Lys Val Ala Ser Gly Lys Tyr Thr Ala
 145 150 155 160
 Asn Tyr Leu Asp Phe His Pro Asn Glu Leu His Ala Gly Asp Ser Gly
 165 170 175
 Thr Phe Gly Gly Tyr Pro Asp Ile Cys His Asp Lys Ser Trp Asp Gln
 180 185 190
 Tyr Trp Leu Trp Ala Ser Gln Glu Ser Tyr Ala Ala Tyr Leu Arg Ser
 195 200 205
 Ile Gly Ile Asp Ala Trp Arg Phe Asp Tyr Val Lys Gly Tyr Gly Ala
 210 215 220
 Trp Val Val Lys Asp Trp Leu Asn Trp Trp Gly Gly Trp Ala Val Gly
 225 230 235 240
 Glu Tyr Trp Asp Thr Asn Val Asp Ala Leu Asn Trp Ala Tyr Ser
 245 250 255
 Ser Gly Ala Lys Val Phe Asp Phe Pro Leu Tyr Tyr Lys Met Asp Ala
 260 265 270
 Ala Phe Asp Asn Lys Asn Ile Pro Ala Leu Val Glu Ala Leu Lys Asn
 275 280 285
 Gly Gly Thr Val Val Ser Arg Asp Pro Phe Lys Ala Val Thr Phe Val
 290 295 300
 Ala Asn His Asp Thr Asp Ile Ile Trp Asn Lys Tyr Pro Ala Tyr Ala
 305 310 315 320
 Phe Ile Leu Thr Tyr Glu Gly Gln Pro Thr Ile Phe Tyr Arg Asp Tyr
 325 330 335
 Glu Glu Trp Leu Asn Lys Asp Lys Leu Lys Asn Leu Ile Trp Ile His
 340 345 350
 Asp Asn Leu Ala Gly Gly Ser Thr Ser Ile Val Tyr Tyr Asp Ser Asp
 355 360 365
 Glu Met Ile Phe Val Arg Asn Gly Tyr Gly Ser Lys Pro Gly Leu Ile
 370 375 380
 Thr Tyr Ile Asn Leu Gly Ser Ser Lys Val Gly Arg Trp Val Tyr Val
 385 390 395 400
 Pro Lys Phe Ala Gly Ala Cys Ile His Glu Tyr Thr Gly Asn Leu Gly
 405 410 415
 Gly Trp Val Asp Lys Tyr Val Tyr Ser Ser Gly Trp Val Tyr Leu Glu
 420 425 430
 Ala Pro Ala Tyr Asp Pro Ala Asn Gly Gln Tyr Gly Tyr Ser Val Trp

435
Ser Tyr Cys Gly Val Gly
450

440

445 -

<210> 14
<211> 460
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 14
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Ala Thr Ser Ala Lys Tyr Leu Glu Leu Glu Glu Gly Gly Val Ile Met
20 25 30
Gln Ala Phe Tyr Trp Asp Val Pro Ser Gly Gly Ile Trp Trp Asp Thr
35 40 45
Ile Arg Gln Lys Ile Pro Glu Trp Tyr Asp Ala Gly Ile Ser Ala Ile
50 55 60
Trp Ile Pro Pro Ala Ser Lys Gly Met Ser Gly Gly Tyr Ser Met Gly
65 70 75 80
Tyr Asp Pro Tyr Asp Tyr Phe Asp Leu Gly Glu Tyr Tyr Gln Lys Gly
85 90 95
Thr Val Glu Thr Arg Phe Gly Ser Lys Gln Glu Leu Ile Asn Met Ile
100 105 110
Asn Thr Ala His Ala Tyr Gly Ile Lys Val Ile Ala Asp Ile Val Ile
115 120 125
Asn His Arg Ala Gly Gly Asp Leu Glu Trp Asn Pro Phe Val Gly Asp
130 135 140
Tyr Thr Trp Thr Asp Phe Ser Lys Val Ala Ser Gly Lys Tyr Thr Ala
145 150 155 160
Asn Tyr Leu Asp Phe His Pro Asn Glu Leu His Ala Gly Asp Ser Gly
165 170 175
Thr Phe Gly Gly Tyr Pro Asp Ile Cys His Asp Lys Ser Trp Asp Gln
180 185 190
Tyr Trp Leu Trp Ala Ser Gln Glu Ser Tyr Ala Ala Tyr Leu Arg Ser
195 200 205
Ile Gly Ile Asp Ala Trp Arg Phe Asp Tyr Val Lys Gly Tyr Gly Ala
210 215 220
Trp Val Val Lys Asp Trp Leu Asn Trp Trp Gly Gly Trp Ala Val Gly
225 230 235 240
Glu Tyr Trp Asp Thr Asn Val Asp Ala Leu Leu Asn Trp Ala Tyr Ser
245 250 255
Ser Gly Ala Lys Val Phe Asp Phe Pro Leu Tyr Tyr Lys Met Asp Ala
260 265 270
Ala Phe Asp Asn Lys Asn Ile Pro Ala Leu Val Glu Ala Leu Lys Asn
275 280 285
Gly Gly Thr Val Val Ser Arg Asp Pro Phe Lys Ala Val Thr Phe Val
290 295 300
Ala Asn His Asp Thr Asp Ile Ile Trp Asn Lys Tyr Pro Ala Tyr Ala
305 310 315 320
Phe Ile Leu Thr Tyr Glu Gly Gln Pro Thr Ile Phe Tyr Arg Asp Tyr
325 330 335
Glu Glu Trp Leu Asn Lys Asp Lys Leu Lys Asn Leu Ile Trp Ile His
340 345 350

Asp Asn Leu Ala Gly Gly Ser Thr Ser Ile Val Tyr Tyr Asp Ser Asp
 355 360 365
 Glu Met Ile Phe Val Arg Asn Gly Tyr Gly Ser Lys Pro Gly Leu Ile
 370 375 380
 Thr Tyr Ile Asn Leu Gly Ser Ser Lys Val Gly Arg Trp Val Tyr Val
 385 390 395 400
 Pro Lys Phe Ala Gly Ala Cys Ile His Glu Tyr Thr Gly Asn Leu Gly
 405 410 415
 Gly Trp Val Asp Lys Tyr Val Tyr Ser Ser Gly Trp Val Tyr Leu Glu
 420 425 430
 Ala Pro Ala Tyr Asp Pro Ala Asn Gly Gln Tyr Gly Tyr Ser Val Trp
 435 440 445
 Ser Tyr Cys Gly Val Gly Ser Glu Lys Asp Glu Leu
 450 455 460

<210> 15
 <211> 518
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 15
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 Leu Arg Gly Ala Arg Ala Ser Ala Ala Asp Thr Leu Ser Met Arg
 35 40 45
 Thr Ser Ala Arg Ala Ala Pro Arg His Gln His Gln Gln Ala Arg Arg
 50 55 60
 Gly Ala Arg Phe Pro Ser Leu Val Val Cys Ala Ser Ala Gly Ala Met
 65 70 75 80
 Ala Lys Tyr Leu Glu Leu Glu Glu Gly Gly Val Ile Met Gln Ala Phe
 85 90 95
 Tyr Trp Asp Val Pro Ser Gly Gly Ile Trp Trp Asp Thr Ile Arg Gln
 100 105 110
 Lys Ile Pro Glu Trp Tyr Asp Ala Gly Ile Ser Ala Ile Trp Ile Pro
 115 120 125
 Pro Ala Ser Lys Gly Met Ser Gly Gly Tyr Ser Met Gly Tyr Asp Pro
 130 135 140
 Tyr Asp Tyr Phe Asp Leu Gly Glu Tyr Tyr Gln Lys Gly Thr Val Glu
 145 150 155 160
 Thr Arg Phe Gly Ser Lys Gln Glu Leu Ile Asn Met Ile Asn Thr Ala
 165 170 175
 His Ala Tyr Gly Ile Lys Val Ile Ala Asp Ile Val Ile Asn His Arg
 180 185 190
 Ala Gly Gly Asp Leu Glu Trp Asn Pro Phe Val Gly Asp Tyr Thr Trp
 195 200 205
 Thr Asp Phe Ser Lys Val Ala Ser Gly Lys Tyr Thr Ala Asn Tyr Leu
 210 215 220
 Asp Phe His Pro Asn Glu Leu His Ala Gly Asp Ser Gly Thr Phe Gly
 225 230 235 240
 Gly Tyr Pro Asp Ile Cys His Asp Lys Ser Trp Asp Gln Tyr Trp Leu
 245 250 255
 Trp Ala Ser Gln Glu Ser Tyr Ala Ala Tyr Leu Arg Ser Ile Gly Ile

260	265	270
Asp Ala Trp Arg Phe Asp Tyr Val Lys Gly Tyr Gly Ala Trp Val Val		
275	280	285
Lys Asp Trp Leu Asn Trp Trp Gly Gly Trp Ala Val Gly Glu Tyr Trp		
290	295	300
Asp Thr Asn Val Asp Ala Leu Leu Asn Trp Ala Tyr Ser Ser Gly Ala		
305	310	315
Lys Val Phe Asp Phe Pro Leu Tyr Tyr Lys Met Asp Ala Ala Phe Asp		
320	325	330
Asn Lys Asn Ile Pro Ala Leu Val Glu Ala Leu Lys Asn Gly Gly Thr		
340	345	350
Val Val Ser Arg Asp Pro Phe Lys Ala Val Thr Phe Val Ala Asn His		
355	360	365
Asp Thr Asp Ile Ile Trp Asn Lys Tyr Pro Ala Tyr Ala Phe Ile Leu		
370	375	380
Thr Tyr Glu Gly Gln Pro Thr Ile Phe Tyr Arg Asp Tyr Glu Glu Trp		
385	390	395
Leu Asn Lys Asp Lys Leu Lys Asn Leu Ile Trp Ile His Asp Asn Leu		
400	405	410
Ala Gly Gly Ser Thr Ser Ile Val Tyr Tyr Asp Ser Asp Glu Met Ile		
415	420	425
Phe Val Arg Asn Gly Tyr Gly Ser Lys Pro Gly Leu Ile Thr Tyr Ile		
430	435	440
Asn Leu Gly Ser Ser Lys Val Gly Arg Trp Val Tyr Val Pro Lys Phe		
445	450	455
Ala Gly Ala Cys Ile His Glu Tyr Thr Gly Asn Leu Gly Gly Trp Val		
460	465	470
Asp Lys Tyr Val Tyr Ser Ser Gly Trp Val Tyr Leu Glu Ala Pro Ala		
475	480	485
Tyr Asp Pro Ala Asn Gly Gln Tyr Gly Tyr Ser Val Trp Ser Tyr Cys		
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Gly Val Gly Thr Ser Ile		
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515		

<210> 16
 <211> 820
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 16
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35 40 45
Thr Ser Ala Arg Ala Ala Pro Arg His Gln His Gln Gln Ala Arg Arg
50 55 60
Gly Ala Arg Phe Pro Ser Leu Val Val Cys Ala Ser Ala Gly Ala Met
65 70 75 80
Ala Lys Tyr Leu Glu Leu Glu Gly Gly Val Ile Met Gln Ala Phe
85 90 95
Tyr Trp Asp Val Pro Ser Gly Gly Ile Trp Trp Asp Thr Ile Arg Gln
100 105 110

Lys	Ile	Pro	Glu	Trp	Tyr	Asp	Ala	Gly	Ile	Ser	Ala	Ile	Trp	Ile	Pro
		115					120					125			
Pro	Ala	Ser	Lys	Gly	Met	Ser	Gly	Gly	Tyr	Ser	Met	Gly	Tyr	Asp	Pro
		130					135				140				
Tyr	Asp	Tyr	Phe	Asp	Leu	Gly	Glu	Tyr	Tyr	Gln	Lys	Gly	Thr	Val	Glu
145					150					155					160
Thr	Arg	Phe	Gly	Ser	Lys	Gln	Glu	Leu	Ile	Asn	Met	Ile	Asn	Thr	Ala
				165					170					175	
His	Ala	Tyr	Gly	Ile	Lys	Val	Ile	Ala	Asp	Ile	Val	Ile	Asn	His	Arg
			180					185					190		
Ala	Gly	Gly	Asp	Leu	Glu	Trp	Asn	Pro	Phe	Val	Gly	Asp	Tyr	Thr	Trp
			195				200					205			
Thr	Asp	Phe	Ser	Lys	Val	Ala	Ser	Gly	Lys	Tyr	Thr	Ala	Asn	Tyr	Leu
						215					220				
Asp	Phe	His	Pro	Asn	Glu	Leu	His	Ala	Gly	Asp	Ser	Gly	Thr	Phe	Gly
225					230					235					240
Gly	Tyr	Pro	Asp	Ile	Cys	His	Asp	Lys	Ser	Trp	Asp	Gln	Tyr	Trp	Leu
				245					250					255	
Trp	Ala	Ser	Gln	Glu	Ser	Tyr	Ala	Ala	Tyr	Leu	Arg	Ser	Ile	Gly	Ile
			260					265					270		
Asp	Ala	Trp	Arg	Phe	Asp	Tyr	Val	Lys	Gly	Tyr	Gly	Ala	Trp	Val	Val
			275				280					285			
Lys	Asp	Trp	Leu	Asn	Trp	Trp	Gly	Gly	Trp	Ala	Val	Gly	Glu	Tyr	Trp
					295					300					
Asp	Thr	Asn	Val	Asp	Ala	Leu	Leu	Asn	Trp	Ala	Tyr	Ser	Ser	Gly	Ala
305					310					315					320
Lys	Val	Phe	Asp	Phe	Pro	Leu	Tyr	Tyr	Lys	Met	Asp	Ala	Ala	Phe	Asp
				325					330					335	
Asn	Lys	Asn	Ile	Pro	Ala	Leu	Val	Glu	Ala	Leu	Lys	Asn	Gly	Gly	Thr
			340					345					350		
Val	Val	Ser	Arg	Asp	Pro	Phe	Lys	Ala	Val	Thr	Phe	Val	Ala	Asn	His
			355				360					365			
Asp	Thr	Asp	Ile	Ile	Trp	Asn	Lys	Tyr	Pro	Ala	Tyr	Ala	Phe	Ile	Leu
					375					380					
Thr	Tyr	Glu	Gly	Gln	Pro	Thr	Ile	Phe	Tyr	Arg	Asp	Tyr	Glu	Glu	Trp
385					390					395					400
Leu	Asn	Lys	Asp	Lys	Leu	Lys	Asn	Leu	Ile	Trp	Ile	His	Asp	Asn	Leu
				405					410					415	
Ala	Gly	Gly	Ser	Thr	Ser	Ile	Val	Tyr	Trp	Asp	Ser	Asp	Glu	Met	Ile
				420				425					430		
Phe	Val	Arg	Asn	Gly	Tyr	Gly	Ser	Lys	Pro	Gly	Leu	Ile	Thr	Tyr	Ile
			435				440					445			
Asn	Leu	Gly	Ser	Ser	Lys	Val	Gly	Arg	Trp	Val	Tyr	Val	Pro	Lys	Phe
					455					460					
Ala	Gly	Ala	Cys	Ile	His	Glu	Tyr	Thr	Gly	Asn	Leu	Gly	Gly	Trp	Val
465					470					475					480
Asp	Lys	Tyr	Val	Tyr	Ser	Ser	Gly	Trp	Val	Tyr	Leu	Glu	Ala	Pro	Ala
				485					490					495	
Tyr	Asp	Pro	Ala	Asn	Gly	Gln	Tyr	Gly	Tyr	Ser	Val	Trp	Ser	Tyr	Cys
				500				505					510		
Gly	Val	Gly	Thr	Ser	Ile	Ala	Gly	Ile	Leu	Glu	Ala	Asp	Arg	Val	Leu
						520						525			
Thr	Val	Ser	Pro	Tyr	Tyr	Ala	Glu	Glu	Leu	Ile	Ser	Gly	Ile	Ala	Arg
						535					540				
Gly	Cys	Glu	Leu	Asp	Asn	Ile	Met	Arg	Leu	Thr	Gly	Ile	Thr	Gly	Ile
545					550					555					560
Val	Asn	Gly	Met	Asp	Val	Ser	Glu	Trp	Asp	Pro	Ser	Arg	Asp	Lys	Tyr
				565					570					575	

Ile Ala Val Lys Tyr Asp Val Ser Thr Ala Val Glu Ala Lys Ala Leu
 580 585 590
 Asn Lys Glu Ala Leu Gln Ala Glu Val Gly Leu Pro Val Asp Arg Asn
 595 600 605
 Ile Pro Leu Val Ala Phe Ile Gly Arg Leu Glu Glu Gln Lys Gly Pro
 610 615 620
 Asp Val Met Ala Ala Ala Ile Pro Gln Leu Met Glu Met Val Glu Asp
 625 630 635 640
 Val Gln Ile Val Leu Leu Gly Thr Gly Lys Lys Lys Phe Glu Arg Met
 645 650 655
 Leu Met Ser Ala Glu Glu Lys Phe Pro Gly Lys Val Arg Ala Val Val
 660 665 670
 Lys Phe Asn Ala Ala Leu Ala His Ile Met Ala Gly Ala Asp Val
 675 680 685
 Leu Ala Val Thr Ser Arg Phe Glu Pro Cys Gly Leu Ile Gln Leu Gln
 690 695 700
 Gly Met Arg Tyr Gly Thr Pro Cys Ala Cys Ala Ser Thr Gly Gly Leu
 705 710 715 720
 Val Asp Thr Ile Ile Glu Gly Lys Thr Gly Phe His Met Gly Arg Leu
 725 730 735
 Ser Val Asp Cys Asn Val Val Glu Pro Ala Asp Val Lys Lys Val Ala
 740 745 750
 Thr Thr Leu Gln Arg Ala Ile Lys Val Val Gly Thr Pro Ala Tyr Glu
 755 760 765
 Glu Met Val Arg Asn Cys Met Ile Gln Asp Leu Ser Trp Lys Gly Pro
 770 775 780
 Ala Lys Asn Trp Glu Asn Val Leu Leu Ser Leu Gly Val Ala Gly Gly
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 Val Ala Ala Pro
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<210> 17
 <211> 19
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 17
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 Ala Thr Ser

<210> 18
 <211> 444
 <212> PRT
 <213> *Thermotoga maritima*

<400> 18
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 1 5 10 15
 Glu Ser Thr Asn Pro Leu Ala Phe Arg Phe Tyr Asp Pro Asn Glu Val

<210>	19
<211>	1335
<212>	DNA

<213> *Thermotoga maritima*

<400> 19

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cacctcaagt tctcgtggc cttctggcac accttcgtga acgagggccg cgaccggttc 180
ggcgaccoga ccgcgagcg ccggtggaac cgcttctccg acccgatgga caaggccttc 240
gcccgcgtgg acgcccctct cgagttctgc gagaagctca acatcgagta cttctgcttc 300
cacgaccgag acatcgcccc ggagggaag accctccgag agaccaacaa gatcctcgac 360
aaggtggtgg agcgcatcaa ggagcgcatg aaggactcca acgtgaagct cctctggggc 420
accgccaacc tcttctccca ccgcgctac atgcacggcg ccgccaccac ctgctccgcc 480
gacgtgttcg cctacgcgc cgcccaggtg aagaaggccc tggagatcac caaggagctg 540
ggcggcgagg gctacgtgtt ctggggcggc cgcgagggtc acgagaccct cctcaacacc 600
gacctcggcc tggagctgga gaacctcgcc cgcttctctc gcatggccgt ggagtacgcc 660
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caccagtagc acttcgacgt ggccaccgcc tacgccttcc tcaagaacca cggcctcgac 780
gagtacttca agttcaacat cgaggccaac cagccacccc tcgcccggcca cacttccag 840
cacgagctgc gcatggcccg catcctcggc aagctcggtt ccacgacgc caaccagggc 900
gacctctctc tcggctggga caccgaccag ttcccagcca acatctacga caccacctc 960
gccatgtacg aggtgatcaa ggccggcggc ttaccaagg gcggcctcaa cttcgacgcc 1020
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ggcaagaccg acttcgagaa gctggaggag tacatcatcg acaaggagga catcgagctg 1260
ccgtccggca agcaggatga cctggagtc ctcctcaact cctacatcgt gaagaccatc 1320
gccgagctgc gctga                                     1335

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<210> 20

<211> 444

<212> PRT

<213> *Thermotoga neapolitana*

<400> 20

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Ile Asp Gly Lys Pro Leu Lys Asp His Leu Lys Phe Ser Val Ala Phe
35     40     45
Trp His Thr Phe Val Asn Glu Gly Arg Asp Pro Phe Gly Asp Pro Thr
50     55     60
Ala Asp Arg Pro Trp Asn Arg Tyr Thr Asp Pro Met Asp Lys Ala Phe
65     70     75     80
Ala Arg Val Asp Ala Leu Phe Glu Phe Cys Glu Lys Leu Asn Ile Glu
85     90     95
Tyr Phe Cys Phe His Asp Arg Asp Ile Ala Pro Glu Gly Lys Thr Leu
100    105    110
Arg Glu Thr Asn Lys Ile Leu Asp Lys Val Val Glu Arg Ile Lys Glu
115    120    125
Arg Met Lys Asp Ser Asn Val Lys Leu Leu Trp Gly Thr Ala Asn Leu
130    135    140
Phe Ser His Pro Arg Tyr Met His Gly Ala Ala Thr Thr Cys Ser Ala
145    150    155    160
Asp Val Phe Ala Tyr Ala Ala Ala Gln Val Lys Lys Ala Leu Glu Ile
165    170    175
Thr Lys Glu Leu Gly Gly Glu Gly Tyr Val Phe Trp Gly Gly Arg Glu
180    185    190
Gly Tyr Glu Thr Leu Leu Asn Thr Asp Leu Gly Phe Glu Leu Glu Asn

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195	200	205
Leu Ala Arg Phe Leu Arg Met Ala Val Asp Tyr Ala Lys Arg Ile Gly		
210	215	220
Phe Thr Gly Gln Phe Leu Ile Glu Pro Lys Pro Lys Glu Pro Thr Lys		
225	230	235
His Gln Tyr Asp Phe Asp Val Ala Thr Ala Tyr Ala Phe Leu Lys Ser		
245	250	255
His Gly Leu Asp Glu Tyr Phe Lys Phe Asn Ile Glu Ala Asn His Ala		
260	265	270
Thr Leu Ala Gly His Thr Phe Gln His Glu Leu Arg Met Ala Arg Ile		
275	280	285
Leu Gly Lys Leu Gly Ser Ile Asp Ala Asn Gln Gly Asp Leu Leu Leu		
290	295	300
Gly Trp Asp Thr Asp Gln Phe Pro Thr Asn Val Tyr Asp Thr Thr Leu		
305	310	315
Ala Met Tyr Glu Val Ile Lys Ala Gly Gly Phe Thr Lys Gly Gly Leu		
325	330	335
Asn Phe Asp Ala Lys Val Arg Arg Ala Ser Tyr Lys Val Glu Asp Leu		
340	345	350
Phe Ile Gly His Ile Ala Gly Met Asp Thr Phe Ala Leu Gly Phe Lys		
355	360	365
Val Ala Tyr Lys Leu Val Lys Asp Gly Val Leu Asp Lys Phe Ile Glu		
370	375	380
Glu Lys Tyr Arg Ser Phe Arg Glu Gly Ile Gly Arg Asp Ile Val Glu		
385	390	395
Gly Lys Val Asp Phe Glu Lys Leu Glu Glu Tyr Ile Ile Asp Lys Glu		
405	410	415
Thr Ile Glu Leu Pro Ser Gly Lys Gln Glu Tyr Leu Glu Ser Leu Ile		
420	425	430
Asn Ser Tyr Ile Val Lys Thr Ile Leu Glu Leu Arg		
435	440	

<210> 21
 <211> 1335
 <212> DNA
 <213> Thermotoga neapolitana

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 caccctcaagt tctccgtggc cttctggcac accttcgtga acgagggccg cgaccggttc 180
 ggcgacccga ccgcccagcg cccgtggaac cgctacaccg acccgatgga caaggccttc 240
 gccgcgctgg acgcctctt cgagttctgc gagaagctca acatcgagta cttctgcttc 300
 caccgaccg acatcgcccc ggagggcaag accctccgag agaccaacaa gatcctcgac 360
 aaggtggtgg agcgcacaa ggagcgcacg aaggactcca acgtgaagct cctctggggc 420
 accgccaacc tcttctccca cccgcgctac atgcacggcg ccgccaccac ctgctccgcc 480
 gacgtgttcg cctacgcccgc cgcccagggtg aagaaggccc tggagatcac caaggagctg 540
 ggcggcgagg gctacgtgtt ctggggcgggc cgcgagggct acgagaccct cctcaacacc 600
 gacctcggct tcgagctgga gaacctcgcc cgcttccctc gcatggccgt ggactacgcc 660
 aagcgcacg gcttcaccgg ccagttctct atcgagccga agccgaagga gccgaccaag 720
 caccagtagc acttcgacgt ggccaaccgc tacgccttcc tcaagtccca cggcctcgac 780
 gactacttca agttcaacat cgaggccaac cagccacccc tcgccggcca cacttccag 840
 caccagctgc gcatggcccg catcctcggc aagctcggct ccacgacgc caaccagggc 900
 gacctcctcc tcggctggga caccgaccag ttcccgaaca acgtgtacga caccaccctc 960
 gccatgtacg aggtgatcaa ggccggcgggc ttaccacaag gcggcctcaa cttcgacgcc 1020
 aaggtgcgcc gcgcctccta caaggtggag gacctcttca tcggccacat cgccggcatg 1080
 gacaccttcg ccctcggcct caaggtggcc tacaagctcg tgaaggacgg cgtgctcgac 1140

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aagttcatcg aggagaagta ccgctccttc cgcgagggca tcggccgcga catcgtggag 1200
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ccgtccggca agcaggagta cctggagtcc ctcatcaact cctacatcgt gaagaccatc 1320
ctggagctgc gctga 1335

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<210> 22
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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 22
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<210> 23
 <211> 29
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 23
 agctaagctt cagggcgcgg ccacgttct 29

<210> 24
 <211> 825
 <212> PRT
 <213> Artificial Sequence

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 Thr Gly Glu Asp Asp Phe Gly Lys Val Ala Val Val Lys Leu Pro Met
 35 40 45
 Asp Leu Thr Lys Val Gly Ile Ile Val Arg Leu Asn Glu Trp Gln Ala
 50 55 60
 Lys Asp Val Ala Lys Asp Arg Phe Ile Glu Ile Lys Asp Gly Lys Ala
 65 70 75 80
 Glu Val Trp Ile Leu Gln Gly Val Glu Glu Ile Phe Tyr Glu Lys Pro
 85 90 95
 Asp Thr Ser Pro Arg Ile Phe Phe Ala Gln Ala Arg Ser Asn Lys Val
 100 105 110
 Ile Glu Ala Phe Leu Thr Asn Pro Val Asp Thr Lys Lys Lys Glu Leu
 115 120 125
 Phe Lys Val Thr Val Asp Gly Lys Glu Ile Pro Val Ser Arg Val Glu
 130 135 140
 Lys Ala Asp Pro Thr Asp Ile Asp Val Thr Asn Tyr Val Arg Ile Val
 145 150 155 160
 Leu Ser Glu Ser Leu Lys Glu Glu Asp Leu Arg Lys Asp Val Glu Leu
 165 170 175

Ile	Ile	Glu	Gly	Tyr	Lys	Pro	Ala	Arg	Val	Ile	Met	Met	Glu	Ile	Leu
			180					185					190		
Asp	Asp	Tyr	Tyr	Tyr	Asp	Gly	Glu	Leu	Gly	Ala	Val	Tyr	Ser	Pro	Glu
		195					200					205			
Lys	Thr	Ile	Phe	Arg	Val	Trp	Ser	Pro	Val	Ser	Lys	Trp	Val	Lys	Val
	210					215					220				
Leu	Leu	Phe	Lys	Asn	Gly	Glu	Asp	Thr	Glu	Pro	Tyr	Gln	Val	Val	Asn
225					230					235					240
Met	Glu	Tyr	Lys	Gly	Asn	Gly	Val	Trp	Glu	Ala	Val	Val	Glu	Gly	Asp
				245					250					255	
Leu	Asp	Gly	Val	Phe	Tyr	Leu	Tyr	Gln	Leu	Glu	Asn	Tyr	Gly	Lys	Ile
			260					265					270		
Arg	Thr	Thr	Val	Asp	Pro	Tyr	Ser	Lys	Ala	Val	Tyr	Ala	Asn	Asn	Gln
		275					280					285			
Glu	Ser	Ala	Val	Val	Asn	Leu	Ala	Arg	Thr	Asn	Pro	Glu	Gly	Trp	Glu
	290					295					300				
Asn	Asp	Arg	Gly	Pro	Lys	Ile	Glu	Gly	Tyr	Glu	Asp	Ala	Ile	Ile	Tyr
305					310					315					320
Glu	Ile	His	Ile	Ala	Asp	Ile	Thr	Gly	Leu	Glu	Asn	Ser	Gly	Val	Lys
				325					330					335	
Asn	Lys	Gly	Leu	Tyr	Leu	Gly	Leu	Thr	Glu	Glu	Asn	Thr	Lys	Ala	Pro
			340					345					350		
Gly	Gly	Val	Thr	Thr	Gly	Leu	Ser	His	Leu	Val	Glu	Leu	Gly	Val	Thr
		355				360						365			
His	Val	His	Ile	Leu	Pro	Phe	Phe	Asp	Phe	Tyr	Thr	Gly	Asp	Glu	Leu
	370					375					380				
Asp	Lys	Asp	Phe	Glu	Lys	Tyr	Tyr	Asn	Trp	Gly	Tyr	Asp	Pro	Tyr	Leu
385					390					395					400
Phe	Met	Val	Pro	Glu	Gly	Arg	Tyr	Ser	Thr	Asp	Pro	Lys	Asn	Pro	His
				405					410					415	
Thr	Arg	Ile	Arg	Glu	Val	Lys	Glu	Met	Val	Lys	Ala	Leu	His	Lys	His
			420					425					430		
Gly	Ile	Gly	Val	Ile	Met	Asp	Met	Val	Phe	Pro	His	Thr	Tyr	Gly	Ile
		435					440					445			
Gly	Glu	Leu	Ser	Ala	Phe	Asp	Gln	Thr	Val	Pro	Tyr	Tyr	Phe	Tyr	Arg
	450					455					460				
Ile	Asp	Lys	Thr	Gly	Ala	Tyr	Leu	Asn	Glu	Ser	Gly	Cys	Gly	Asn	Val
465					470					475					480
Ile	Ala	Ser	Glu	Arg	Pro	Met	Met	Arg	Lys	Phe	Ile	Val	Asp	Thr	Val
				485					490					495	
Thr	Tyr	Trp	Val	Lys	Glu	Tyr	His	Ile	Asp	Gly	Phe	Arg	Phe	Asp	Gln
			500					505					510		
Met	Gly	Leu	Ile	Asp	Lys	Lys	Thr	Met	Leu	Glu	Val	Glu	Arg	Ala	Leu
		515					520					525			
His	Lys	Ile	Asp	Pro	Thr	Ile	Ile	Leu	Tyr	Gly	Glu	Pro	Trp	Gly	Gly
	530					535					540				
Trp	Gly	Ala	Pro	Ile	Arg	Phe	Gly	Lys	Ser	Asp	Val	Ala	Gly	Thr	His
545					550					555					560
Val	Ala	Ala	Phe	Asn	Asp	Glu	Phe	Arg	Asp	Ala	Ile	Arg	Gly	Ser	Val
				565					570					575	
Phe	Asn	Pro	Ser	Val	Lys	Gly	Phe	Val	Met	Gly	Gly	Tyr	Gly	Lys	Glu
				580				585					590		
Thr	Lys	Ile	Lys	Arg	Gly	Val	Val	Gly	Ser	Ile	Asn	Tyr	Asp	Gly	Lys
		595					600					605			
Leu	Ile	Lys	Ser	Phe	Ala	Leu	Asp	Pro	Glu	Glu	Thr	Ile	Asn	Tyr	Ala
	610					615					620				
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625					630					635					640

Lys Ala Asp Lys Lys Lys Glu Trp Thr Glu Glu Glu Leu Lys Asn Ala
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 Gln Lys Leu Ala Gly Ala Ile Leu Leu Thr Ser Gln Gly Val Pro Phe
 660 665 670
 Leu His Gly Gly Gln Asp Phe Cys Arg Thr Thr Asn Phe Asn Asp Asn
 675 680 685
 Ser Tyr Asn Ala Pro Ile Ser Ile Asn Gly Phe Asp Tyr Glu Arg Lys
 690 695 700
 Leu Gln Phe Ile Asp Val Phe Asn Tyr His Lys Gly Leu Ile Lys Leu
 705 710 715 720
 Arg Lys Glu His Pro Ala Phe Arg Leu Lys Asn Ala Glu Glu Ile Lys
 725 730 735
 Lys His Leu Glu Phe Leu Pro Gly Gly Arg Arg Ile Val Ala Phe Met
 740 745 750
 Leu Lys Asp His Ala Gly Gly Asp Pro Trp Lys Asp Ile Val Val Ile
 755 760 765
 Tyr Asn Gly Asn Leu Glu Lys Thr Thr Tyr Lys Leu Pro Glu Gly Lys
 770 775 780
 Trp Asn Val Val Val Asn Ser Gln Lys Ala Gly Thr Glu Val Ile Glu
 785 790 795 800
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<210> 25

<211> 2478

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 25

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gtggccgtgg  tgaagctccc  gatggacctc  accaagggtg  gcatcatcgt  gcgcctcaac  180
gagtggcagg  cgaaggacgt  ggccaaggac  cgcttcacgc  agatcaagga  cggcaaggcc  240
gaggtgtgga  tactccaggg  cgtggaggag  atcttctacg  agaagccgga  cacctccccg  300
cgcattctct  tcgcccaggc  ccgctccaac  aaggtgatcg  aggccttcct  caccaaccgc  360
gtggacacca  agaagaagga  gctgttcaag  gtgaccgtcg  acggcaagga  gatcccgggtg  420
tcccgcgtgg  agaaggccga  cccgaccgac  atcgacgtga  ccaactacgt  gcgcacgtg  480
ctctccgagt  ccctcaagga  ggaggacctc  cgcaaggacg  tggagctgat  catcgagggc  540
tacaagccgg  cccgcgtgat  catgatggag  atcctcgacg  actactacta  cgacggcgag  600
ctggggggcg  tgtactcccc  ggagaagacc  atcttcgcgc  tgtggtcccc  ggtgtccaag  660
tgggtgaagg  tgctcctctt  caagaacggc  gaggacaccg  agccgtacca  ggtggtgaac  720
atggagtaca  agggcaacgg  cgtgtgggag  gccgtggtgg  agggcgacct  cgacggcggtg  780
ttctacctct  accagctgga  gaactacggc  aagatccgca  ccaccgtgga  cccgtactcc  840
aaggccgtgt  acgccaacaa  ccaggagtct  cgagtgggtg  acctcgcccc  caccaaccgc  900
gagggctggg  agaacgaccg  cggcccgaag  atcgagggtc  acgaggacgc  catcatctac  960
gagatccaca  tcgcccacat  caccggcctg  gagaactccg  gcgtgaagaa  caagggcctc  1020
tacctcggcc  tcaccgagga  gaacaccaag  gccccgggcg  gcgtgaccac  cggcctctcc  1080
cacctcgtgg  agctgggcgt  gacccacgtg  cacatcctcc  cggttcttga  cttctacacc  1140
ggcgacgagc  tggacaagga  cttcgagaag  tactacaact  ggggtacga  cccgtacctc  1200
ttcatggtgc  cggaggggcg  ctactccacc  gaccggaaga  acccgcacac  ccgaattcgc  1260
gaggtgaagg  agatggtgaa  ggccctccac  aagcacggca  tcggcggtgat  catggacatg  1320
gtgttccccg  acacctacgg  catcggcgag  ctgtccgcct  tcgaccagac  cgtgccgtac  1380
  
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tacttctacc gcatcgacaa gaccggcgcc tacctcaacg agtccggctg cggcaacgtg 1440
atcgccctccg agcgcccgat gatgcgcaag ttcatcgtag acaccgtgac ctactgggtg 1500
aaggagtagc acatcgacgg cttccgcttc gaccagatgg gcctcatcga caagaagacc 1560
atgctggagg tggagcgcg cctccacaag atcgaccga ccatcatcct ctacggcgag 1620
ccgtggggcg gctggggggc cccgatccgc ttgggcaagt ccgacgtggc cggcaccac 1680
gtggccgcct tcaacgacga gttccgagac gccatccgcg gctccgtgtt caaccctgcc 1740
gtgaagggtc tctgatggg cggctacggc aaggagacca agatcaagcg cggcgtgggtg 1800
ggctccatca actacgacgg caagctcatc aagtccttcg ccctcgaccg ggaggagacc 1860
atcaactacg ccgcctgcca cgacaaccac accctctggg acaagaacta cctcgccgcc 1920
aaggccgaca agaagaagga gtggaccgag gaggagctga agaacgcccc gaagctcgcc 1980
ggcgccatcc tctcactag tcaggggcgtg ccgttcctcc acggcggcca ggacttctgc 2040
cgcaccacca acttcaacga caactcctac aacgccccga tctccatcaa cggcttcgac 2100
tacgagcgca agctccagtt catcgacgtg ttcaactacc acaagggcct catcaagctc 2160
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ttcctcccg gcgggcgccg catcgtggcc ttcatgctca aggaccacgc cggcggcgac 2280
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gagaaggacg agctgtga

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<210> 26
 <211> 718
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 26

Met	Arg	Val	Leu	Leu	Val	Ala	Leu	Ala	Leu	Leu	Ala	Leu	Ala	Ala	Ser
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Ala	Thr	Ser	Met	Glu	Thr	Ile	Lys	Ile	Tyr	Glu	Asn	Lys	Gly	Val	Tyr
			20					25					30		
Lys	Val	Val	Ile	Gly	Glu	Pro	Phe	Pro	Pro	Ile	Glu	Phe	Pro	Leu	Glu
			35				40					45			
Gln	Lys	Ile	Ser	Ser	Asn	Lys	Ser	Leu	Ser	Glu	Leu	Gly	Leu	Thr	Ile
			50			55					60				
Val	Gln	Gln	Gly	Asn	Lys	Val	Ile	Val	Glu	Lys	Ser	Leu	Asp	Leu	Lys
65					70				75					80	
Glu	His	Ile	Ile	Gly	Leu	Gly	Glu	Lys	Ala	Phe	Glu	Leu	Asp	Arg	Lys
				85					90					95	
Arg	Lys	Arg	Tyr	Val	Met	Tyr	Asn	Val	Asp	Ala	Gly	Ala	Tyr	Lys	Lys
			100					105					110		
Tyr	Gln	Asp	Pro	Leu	Tyr	Val	Ser	Ile	Pro	Leu	Phe	Ile	Ser	Val	Lys
			115				120					125			
Asp	Gly	Val	Ala	Thr	Gly	Tyr	Phe	Phe	Asn	Ser	Ala	Ser	Lys	Val	Ile
			130				135				140				
Phe	Asp	Val	Gly	Leu	Glu	Glu	Tyr	Asp	Lys	Val	Ile	Val	Thr	Ile	Pro
145					150				155					160	
Glu	Asp	Ser	Val	Glu	Phe	Tyr	Val	Ile	Glu	Gly	Pro	Arg	Ile	Glu	Asp
				165					170					175	
Val	Leu	Glu	Lys	Tyr	Thr	Glu	Leu	Thr	Gly	Lys	Pro	Phe	Leu	Pro	Pro
				180				185					190		
Met	Trp	Ala	Phe	Gly	Tyr	Met	Ile	Ser	Arg	Tyr	Ser	Tyr	Tyr	Pro	Gln
							200					205			
Asp	Lys	Val	Val	Glu	Leu	Val	Asp	Ile	Met	Gln	Lys	Glu	Gly	Phe	Arg
							215				220				
Val	Ala	Gly	Val	Phe	Leu	Asp	Ile	His	Tyr	Met	Asp	Ser	Tyr	Lys	Leu

225					230					235				240
Phe	Thr	Trp	His	Pro	Tyr	Arg	Phe	Pro	Glu	Pro	Lys	Lys	Leu	Ile
				245					250					255
Glu	Leu	His	Lys	Arg	Asn	Val	Lys	Leu	Ile	Thr	Ile	Val	Asp	His
			260					265					270	
Ile	Arg	Val	Asp	Gln	Asn	Tyr	Ser	Pro	Phe	Leu	Ser	Gly	Met	Gly
		275					280					285		Lys
Phe	Cys	Glu	Ile	Glu	Ser	Gly	Glu	Leu	Phe	Val	Gly	Lys	Met	Trp
	290					295					300			Pro
Gly	Thr	Thr	Val	Tyr	Pro	Asp	Phe	Phe	Arg	Glu	Asp	Thr	Arg	Glu
305					310					315				320
Trp	Ala	Gly	Leu	Ile	Ser	Glu	Trp	Leu	Ser	Gln	Gly	Val	Asp	Gly
				325					330					335
Trp	Leu	Asp	Met	Asn	Glu	Pro	Thr	Asp	Phe	Ser	Arg	Ala	Ile	Glu
		340						345					350	Ile
Arg	Asp	Val	Leu	Ser	Ser	Leu	Pro	Val	Gln	Phe	Arg	Asp	Asp	Arg
	355						360					365		Leu
Val	Thr	Thr	Phe	Pro	Asp	Asn	Val	Val	His	Tyr	Leu	Arg	Gly	Lys
	370					375					380			Arg
Val	Lys	His	Glu	Lys	Val	Arg	Asn	Ala	Tyr	Pro	Leu	Tyr	Glu	Ala
385					390					395				400
Ala	Thr	Phe	Lys	Gly	Phe	Arg	Thr	Ser	His	Arg	Asn	Glu	Ile	Phe
			405						410					415
Leu	Ser	Arg	Ala	Gly	Tyr	Ala	Gly	Ile	Gln	Arg	Tyr	Ala	Phe	Ile
			420					425					430	Trp
Thr	Gly	Asp	Asn	Thr	Pro	Ser	Trp	Asp	Asp	Leu	Lys	Leu	Gln	Leu
	435						440					445		Gln
Leu	Val	Leu	Gly	Leu	Ser	Ile	Ser	Gly	Val	Pro	Phe	Val	Gly	Cys
	450					455					460			Asp
Ile	Gly	Gly	Phe	Gln	Gly	Arg	Asn	Phe	Ala	Glu	Ile	Asp	Asn	Ser
465					470					475				480
Asp	Leu	Leu	Val	Lys	Tyr	Tyr	Ala	Leu	Ala	Leu	Phe	Phe	Pro	Phe
			485						490					495
Arg	Ser	His	Lys	Ala	Thr	Asp	Gly	Ile	Asp	Thr	Glu	Pro	Val	Phe
			500					505					510	Leu
Pro	Asp	Tyr	Tyr	Lys	Glu	Lys	Val	Lys	Glu	Ile	Val	Glu	Leu	Arg
	515						520					525		Tyr
Lys	Phe	Leu	Pro	Tyr	Ile	Tyr	Ser	Leu	Ala	Leu	Glu	Ala	Ser	Glu
	530					535					540			Lys
Gly	His	Pro	Val	Ile	Arg	Pro	Leu	Phe	Tyr	Glu	Phe	Gln	Asp	Asp
545					550					555				560
Asp	Met	Tyr	Arg	Ile	Glu	Asp	Glu	Tyr	Met	Val	Gly	Lys	Tyr	Leu
				565					570					575
Tyr	Ala	Pro	Ile	Val	Ser	Lys	Glu	Glu	Ser	Arg	Leu	Val	Thr	Leu
			580					585					590	Pro
Arg	Gly	Lys	Trp	Tyr	Asn	Tyr	Trp	Asn	Gly	Glu	Ile	Ile	Asn	Gly
	595						600					605		Lys
Ser	Val	Val	Lys	Ser	Thr	His	Glu	Leu	Pro	Ile	Tyr	Leu	Arg	Glu
	610					615					620			Gly
Ser	Ile	Ile	Pro	Leu	Glu	Gly	Asp	Glu	Leu	Ile	Val	Tyr	Gly	Glu
625					630					635				640
Ser	Phe	Lys	Arg	Tyr	Asp	Asn	Ala	Glu	Ile	Thr	Ser	Ser	Ser	Asn
				645					650					655
Ile	Lys	Phe	Ser	Arg	Glu	Ile	Tyr	Val	Ser	Lys	Leu	Thr	Ile	Thr
			660					665					670	Ser
Glu	Lys	Pro	Val	Ser	Lys	Ile	Ile	Val	Asp	Asp	Ser	Lys	Glu	Ile
	675					680						685		Gln
Val	Glu	Lys	Thr	Met	Gln	Asn	Thr	Tyr	Val	Ala	Lys	Ile	Asn	Gln
														Lys

690	Ile	Arg	Gly	Lys	Ile	Asn	Leu	Glu	Ser	Glu	Lys	Asp	Glu	Leu
705					710						715			

<210> 27
 <211> 712
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 27
 Met Arg Val Leu Leu Val Ala Leu Ala Leu Leu Ala Leu Ala Ala Ser
 1 5 10 15
 Ala Thr Ser Met Glu Thr Ile Lys Ile Tyr Glu Asn Lys Gly Val Tyr
 20 25 30
 Lys Val Val Ile Gly Glu Pro Phe Pro Pro Ile Glu Phe Pro Leu Glu
 35 40 45
 Gln Lys Ile Ser Ser Asn Lys Ser Leu Ser Glu Leu Gly Leu Thr Ile
 50 55 60
 Val Gln Gln Gly Asn Lys Val Ile Val Glu Lys Ser Leu Asp Leu Lys
 65 70 75 80
 Glu His Ile Ile Gly Leu Gly Glu Lys Ala Phe Glu Leu Asp Arg Lys
 85 90 95
 Arg Lys Arg Tyr Val Met Tyr Asn Val Asp Ala Gly Ala Tyr Lys Lys
 100 105 110
 Tyr Gln Asp Pro Leu Tyr Val Ser Ile Pro Leu Phe Ile Ser Val Lys
 115 120 125
 Asp Gly Val Ala Thr Gly Tyr Phe Phe Asn Ser Ala Ser Lys Val Ile
 130 135 140
 Phe Asp Val Gly Leu Glu Glu Tyr Asp Lys Val Ile Val Thr Ile Pro
 145 150 155 160
 Glu Asp Ser Val Glu Phe Tyr Val Ile Glu Gly Pro Arg Ile Glu Asp
 165 170 175
 Val Leu Glu Lys Tyr Thr Glu Leu Thr Gly Lys Pro Phe Leu Pro Pro
 180 185 190
 Met Trp Ala Phe Gly Tyr Met Ile Ser Arg Tyr Ser Tyr Tyr Pro Gln
 195 200 205
 Asp Lys Val Val Glu Leu Val Asp Ile Met Gln Lys Glu Gly Phe Arg
 210 215 220
 Val Ala Gly Val Phe Leu Asp Ile His Tyr Met Asp Ser Tyr Lys Leu
 225 230 235 240
 Phe Thr Trp His Pro Tyr Arg Phe Pro Glu Pro Lys Lys Leu Ile Asp
 245 250 255
 Glu Leu His Lys Arg Asn Val Lys Leu Ile Thr Ile Val Asp His Gly
 260 265 270
 Ile Arg Val Asp Gln Asn Tyr Ser Pro Phe Leu Ser Gly Met Gly Lys
 275 280 285
 Phe Cys Glu Ile Glu Ser Gly Glu Leu Phe Val Gly Lys Met Trp Pro
 290 295 300
 Gly Thr Thr Val Tyr Pro Asp Phe Phe Arg Glu Asp Thr Arg Glu Trp
 305 310 315 320
 Trp Ala Gly Leu Ile Ser Glu Trp Leu Ser Gln Gly Val Asp Gly Ile
 325 330 335
 Trp Leu Asp Met Asn Glu Pro Thr Asp Phe Ser Arg Ala Ile Glu Ile
 340 345 350

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Arg Asp Val Leu Ser Ser Leu Pro Val Gln Phe Arg Asp Asp Arg Leu
355 360 365
Val Thr Thr Phe Pro Asp Asn Val Val His Tyr Leu Arg Gly Lys Arg
370 375 380
Val Lys His Glu Lys Val Arg Asn Ala Tyr Pro Leu Tyr Glu Ala Met
385 390 395 400
Ala Thr Phe Lys Gly Phe Arg Thr Ser His Arg Asn Glu Ile Phe Ile
405 410 415
Leu Ser Arg Ala Gly Tyr Ala Gly Ile Gln Arg Tyr Ala Phe Ile Trp
420 425 430
Thr Gly Asp Asn Thr Pro Ser Trp Asp Asp Leu Lys Leu Gln Leu Gln
435 440 445
Leu Val Leu Gly Leu Ser Ile Ser Gly Val Pro Phe Val Gly Cys Asp
450 455 460
Ile Gly Gly Phe Gln Gly Arg Asn Phe Ala Glu Ile Asp Asn Ser Met
465 470 475 480
Asp Leu Leu Val Lys Tyr Tyr Ala Leu Ala Leu Phe Phe Pro Phe Tyr
485 490 495
Arg Ser His Lys Ala Thr Asp Gly Ile Asp Thr Glu Pro Val Phe Leu
500 505 510
Pro Asp Tyr Tyr Lys Glu Lys Val Lys Glu Ile Val Glu Leu Arg Tyr
515 520 525
Lys Phe Leu Pro Tyr Ile Tyr Ser Leu Ala Leu Glu Ala Ser Glu Lys
530 535 540
Gly His Pro Val Ile Arg Pro Leu Phe Tyr Glu Phe Gln Asp Asp Asp
545 550 555 560
Asp Met Tyr Arg Ile Glu Asp Glu Tyr Met Val Gly Lys Tyr Leu Leu
565 570 575
Tyr Ala Pro Ile Val Ser Lys Glu Glu Ser Arg Leu Val Thr Leu Pro
580 585 590
Arg Gly Lys Trp Tyr Asn Tyr Trp Asn Gly Glu Ile Ile Asn Gly Lys
595 600 605
Ser Val Val Lys Ser Thr His Glu Leu Pro Ile Tyr Leu Arg Glu Gly
610 615 620
Ser Ile Ile Pro Leu Glu Gly Asp Glu Leu Ile Val Tyr Gly Glu Thr
625 630 635 640
Ser Phe Lys Arg Tyr Asp Asn Ala Glu Ile Thr Ser Ser Ser Asn Glu
645 650 655
Ile Lys Phe Ser Arg Glu Ile Tyr Val Ser Lys Leu Thr Ile Thr Ser
660 665 670
Glu Lys Pro Val Ser Lys Ile Ile Val Asp Asp Ser Lys Glu Ile Gln
675 680 685
Val Glu Lys Thr Met Gln Asn Thr Tyr Val Ala Lys Ile Asn Gln Lys
690 695 700
Ile Arg Gly Lys Ile Asn Leu Glu
705 710

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<210> 28
 <211> 469
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 28
 Met Arg Val Leu Leu Val Ala Leu Ala Leu Leu Ala Leu Ala Ala Ser

1				5				10				15			
Ala	Thr	Ser	Met	Ala	Glu	Phe	Phe	Pro	Glu	Ile	Pro	Lys	Ile	Gln	Phe
			20					25					30		
Glu	Gly	Lys	Glu	Ser	Thr	Asn	Pro	Leu	Ala	Phe	Arg	Phe	Tyr	Asp	Pro
		35					40					45			
Asn	Glu	Val	Ile	Asp	Gly	Lys	Pro	Leu	Lys	Asp	His	Leu	Lys	Phe	Ser
	50					55					60				
Val	Ala	Phe	Trp	His	Thr	Phe	Val	Asn	Glu	Gly	Arg	Asp	Pro	Phe	Gly
	65				70					75				80	
Asp	Pro	Thr	Ala	Glu	Arg	Pro	Trp	Asn	Arg	Phe	Ser	Asp	Pro	Met	Asp
			85					90					95		
Lys	Ala	Phe	Ala	Arg	Val	Asp	Ala	Leu	Phe	Glu	Phe	Cys	Glu	Lys	Leu
			100					105					110		
Asn	Ile	Glu	Tyr	Phe	Cys	Phe	His	Asp	Arg	Asp	Ile	Ala	Pro	Glu	Gly
		115					120					125			
Lys	Thr	Leu	Arg	Glu	Thr	Asn	Lys	Ile	Leu	Asp	Lys	Val	Val	Glu	Arg
	130					135					140				
Ile	Lys	Glu	Arg	Met	Lys	Asp	Ser	Asn	Val	Lys	Leu	Leu	Trp	Gly	Thr
	145				150					155				160	
Ala	Asn	Leu	Phe	Ser	His	Pro	Arg	Tyr	Met	His	Gly	Ala	Ala	Thr	Thr
			165					170					175		
Cys	Ser	Ala	Asp	Val	Phe	Ala	Tyr	Ala	Ala	Ala	Gln	Val	Lys	Lys	Ala
			180					185					190		
Leu	Glu	Ile	Thr	Lys	Glu	Leu	Gly	Gly	Glu	Gly	Tyr	Val	Phe	Trp	Gly
		195					200					205			
Gly	Arg	Glu	Gly	Tyr	Glu	Thr	Leu	Leu	Asn	Thr	Asp	Leu	Gly	Leu	Glu
	210					215					220				
Leu	Glu	Asn	Leu	Ala	Arg	Phe	Leu	Arg	Met	Ala	Val	Glu	Tyr	Ala	Lys
	225				230					235				240	
Lys	Ile	Gly	Phe	Thr	Gly	Gln	Phe	Leu	Ile	Glu	Pro	Lys	Pro	Lys	Glu
			245					250					255		
Pro	Thr	Lys	His	Gln	Tyr	Asp	Phe	Asp	Val	Ala	Thr	Ala	Tyr	Ala	Phe
			260					265					270		
Leu	Lys	Asn	His	Gly	Leu	Asp	Glu	Tyr	Phe	Lys	Phe	Asn	Ile	Glu	Ala
		275					280					285			
Asn	His	Ala	Thr	Leu	Ala	Gly	His	Thr	Phe	Gln	His	Glu	Leu	Arg	Met
	290					295					300				
Ala	Arg	Ile	Leu	Gly	Lys	Leu	Gly	Ser	Ile	Asp	Ala	Asn	Gln	Gly	Asp
	305				310					315				320	
Leu	Leu	Leu	Gly	Trp	Asp	Thr	Asp	Gln	Phe	Pro	Thr	Asn	Ile	Tyr	Asp
			325					330					335		
Thr	Thr	Leu	Ala	Met	Tyr	Glu	Val	Ile	Lys	Ala	Gly	Gly	Phe	Thr	Lys
		340						345					350		
Gly	Gly	Leu	Asn	Phe	Asp	Ala	Lys	Val	Arg	Arg	Ala	Ser	Tyr	Lys	Val
		355					360					365			
Glu	Asp	Leu	Phe	Ile	Gly	His	Ile	Ala	Gly	Met	Asp	Thr	Phe	Ala	Leu
	370				375						380				
Gly	Phe	Lys	Ile	Ala	Tyr	Lys	Leu	Ala	Lys	Asp	Gly	Val	Phe	Asp	Lys
	385				390					395				400	
Phe	Ile	Glu	Glu	Lys	Tyr	Arg	Ser	Phe	Lys	Glu	Gly	Ile	Gly	Lys	Glu
			405					410					415		
Ile	Val	Glu	Gly	Lys	Thr	Asp	Phe	Glu	Lys	Leu	Glu	Glu	Tyr	Ile	Ile
		420						425					430		
Asp	Lys	Glu	Asp	Ile	Glu	Leu	Pro	Ser	Gly	Lys	Gln	Glu	Tyr	Leu	Glu
		435					440					445			
Ser	Leu	Leu	Asn	Ser	Tyr	Ile	Val	Lys	Thr	Ile	Ala	Glu	Leu	Arg	Ser
	450					455					460				
Glu	Lys	Asp	Glu	Leu											

465

<210> 29
 <211> 469
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 29
 Met Arg Val Leu Leu Val Ala Leu Ala Leu Leu Ala Leu Ala Ala Ser
 1 5 10 15
 Ala Thr Ser Met Ala Glu Phe Phe Pro Glu Ile Pro Lys Val Gln Phe
 20 25 30
 Glu Gly Lys Glu Ser Thr Asn Pro Leu Ala Phe Lys Phe Tyr Asp Pro
 35 40 45
 Glu Glu Ile Ile Asp Gly Lys Pro Leu Lys Asp His Leu Lys Phe Ser
 50 55 60
 Val Ala Phe Trp His Thr Phe Val Asn Glu Gly Arg Asp Pro Phe Gly
 65 70 75 80
 Asp Pro Thr Ala Asp Arg Pro Trp Asn Arg Tyr Thr Asp Pro Met Asp
 85 90 95
 Lys Ala Phe Ala Arg Val Asp Ala Leu Phe Glu Phe Cys Glu Lys Leu
 100 105 110
 Asn Ile Glu Tyr Phe Cys Phe His Asp Arg Asp Ile Ala Pro Glu Gly
 115 120 125
 Lys Thr Leu Arg Glu Thr Asn Lys Ile Leu Asp Lys Val Val Glu Arg
 130 135 140
 Ile Lys Glu Arg Met Lys Asp Ser Asn Val Lys Leu Leu Trp Gly Thr
 145 150 155 160
 Ala Asn Leu Phe Ser His Pro Arg Tyr Met His Gly Ala Ala Thr Thr
 165 170 175
 Cys Ser Ala Asp Val Phe Ala Tyr Ala Ala Ala Gln Val Lys Lys Ala
 180 185 190
 Leu Glu Ile Thr Lys Glu Leu Gly Gly Glu Gly Tyr Val Phe Trp Gly
 195 200 205
 Gly Arg Glu Gly Tyr Glu Thr Leu Leu Asn Thr Asp Leu Gly Phe Glu
 210 215 220
 Leu Glu Asn Leu Ala Arg Phe Leu Arg Met Ala Val Asp Tyr Ala Lys
 225 230 235 240
 Arg Ile Gly Phe Thr Gly Gln Phe Leu Ile Glu Pro Lys Pro Lys Glu
 245 250 255
 Pro Thr Lys His Gln Tyr Asp Phe Asp Val Ala Thr Ala Tyr Ala Phe
 260 265 270
 Leu Lys Ser His Gly Leu Asp Glu Tyr Phe Lys Phe Asn Ile Glu Ala
 275 280 285
 Asn His Ala Thr Leu Ala Gly His Thr Phe Gln His Glu Leu Arg Met
 290 295 300
 Ala Arg Ile Leu Gly Lys Leu Gly Ser Ile Asp Ala Asn Gln Gly Asp
 305 310 315 320
 Leu Leu Leu Gly Trp Asp Thr Asp Gln Phe Pro Thr Asn Val Tyr Asp
 325 330 335
 Thr Thr Leu Ala Met Tyr Glu Val Ile Lys Ala Gly Gly Phe Thr Lys
 340 345 350
 Gly Gly Leu Asn Phe Asp Ala Lys Val Arg Arg Ala Ser Tyr Lys Val
 355 360 365

Glu Asp Leu Phe Ile Gly His Ile Ala Gly Met Asp Thr Phe Ala Leu
 370 375 380
 Gly Phe Lys Val Ala Tyr Lys Leu Val Lys Asp Gly Val Leu Asp Lys
 385 390 395 400
 Phe Ile Glu Glu Lys Tyr Arg Ser Phe Arg Glu Gly Ile Gly Arg Asp
 405 410 415
 Ile Val Glu Gly Lys Val Asp Phe Glu Lys Leu Glu Glu Tyr Ile Ile
 420 425 430
 Asp Lys Glu Thr Ile Glu Leu Pro Ser Gly Lys Gln Glu Tyr Leu Glu
 435 440 445
 Ser Leu Ile Asn Ser Tyr Ile Val Lys Thr Ile Leu Glu Leu Arg Ser
 450 455 460
 Glu Lys Asp Glu Leu
 465

<210> 30
 <211> 463
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 30
 Met Arg Val Leu Leu Val Ala Leu Ala Leu Leu Ala Leu Ala Ala Ser
 1 5 10 15
 Ala Thr Ser Met Ala Glu Phe Phe Pro Glu Ile Pro Lys Val Gln Phe
 20 25 30
 Glu Gly Lys Glu Ser Thr Asn Pro Leu Ala Phe Lys Phe Tyr Asp Pro
 35 40 45
 Glu Glu Ile Ile Asp Gly Lys Pro Leu Lys Asp His Leu Lys Phe Ser
 50 55 60
 Val Ala Phe Trp His Thr Phe Val Asn Glu Gly Arg Asp Pro Phe Gly
 65 70 75 80
 Asp Pro Thr Ala Asp Arg Pro Trp Asn Arg Tyr Thr Asp Pro Met Asp
 85 90 95
 Lys Ala Phe Ala Arg Val Asp Ala Leu Phe Glu Phe Cys Glu Lys Leu
 100 105 110
 Asn Ile Glu Tyr Phe Cys Phe His Asp Arg Asp Ile Ala Pro Glu Gly
 115 120 125
 Lys Thr Leu Arg Glu Thr Asn Lys Ile Leu Asp Lys Val Val Glu Arg
 130 135 140
 Ile Lys Glu Arg Met Lys Asp Ser Asn Val Lys Leu Leu Trp Gly Thr
 145 150 155 160
 Ala Asn Leu Phe Ser His Pro Arg Tyr Met His Gly Ala Thr Thr
 165 170 175
 Cys Ser Ala Asp Val Phe Ala Tyr Ala Ala Gln Val Lys Lys Ala
 180 185 190
 Leu Glu Ile Thr Lys Glu Leu Gly Gly Glu Gly Tyr Val Phe Trp Gly
 195 200 205
 Gly Arg Glu Gly Tyr Glu Thr Leu Leu Asn Thr Asp Leu Gly Phe Glu
 210 215 220
 Leu Glu Asn Leu Ala Arg Phe Leu Arg Met Ala Val Asp Tyr Ala Lys
 225 230 235 240
 Arg Ile Gly Phe Thr Gly Gln Phe Leu Ile Glu Pro Lys Pro Lys Glu
 245 250 255
 Pro Thr Lys His Gln Tyr Asp Phe Asp Val Ala Thr Ala Tyr Ala Phe


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                260                265                270
Leu Lys Ser His Gly Leu Asp Glu Tyr Phe Lys Phe Asn Ile Glu Ala
      275                280                285
Asn His Ala Thr Leu Ala Gly His Thr Phe Gln His Glu Leu Arg Met
      290                295                300
Ala Arg Ile Leu Gly Lys Leu Gly Ser Ile Asp Ala Asn Gln Gly Asp
305                310                315
Leu Leu Leu Gly Trp Asp Thr Asp Gln Phe Pro Thr Asn Val Tyr Asp
      325                330                335
Thr Thr Leu Ala Met Tyr Glu Val Ile Lys Ala Gly Gly Phe Thr Lys
      340                345                350
Gly Gly Leu Asn Phe Asp Ala Lys Val Arg Arg Ala Ser Tyr Lys Val
      355                360                365
Glu Asp Leu Phe Ile Gly His Ile Ala Gly Met Asp Thr Phe Ala Leu
      370                375                380
Gly Phe Lys Val Ala Tyr Lys Leu Val Lys Asp Gly Val Leu Asp Lys
385                390                395
Phe Ile Glu Glu Lys Tyr Arg Ser Phe Arg Glu Gly Ile Gly Arg Asp
      405                410                415
Ile Val Glu Gly Lys Val Asp Phe Glu Lys Leu Glu Glu Tyr Ile Ile
      420                425                430
Asp Lys Glu Thr Ile Glu Leu Pro Ser Gly Lys Gln Glu Tyr Leu Glu
      435                440                445
Ser Leu Ile Asn Ser Tyr Ile Val Lys Thr Ile Leu Glu Leu Arg
      450                455                460

```

<210> 31
 <211> 25
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

```

<400> 31
Met Gly Lys Asn Gly Asn Leu Cys Cys Phe Ser Leu Leu Leu Leu Leu
  1                5                10                15
Leu Ala Gly Leu Ala Ser Gly His Gln
      20                25

```

<210> 32
 <211> 30
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

```

<400> 32
Met Gly Phe Val Leu Phe Ser Gln Leu Pro Ser Phe Leu Leu Val Ser
  1                5                10                15
Thr Leu Leu Leu Phe Leu Val Ile Ser His Ser Cys Arg Ala
      20                25                30

```

<210> 33

<211> 460
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 33
 Met Arg Val Leu Leu Val Ala Leu Ala Leu Leu Ala Leu Ala Ala Ser
 1 5 10 15
 Ala Thr Ser Ala Lys Tyr Leu Glu Leu Glu Gly Gly Val Ile Met
 20 25 30
 Gln Ala Phe Tyr Trp Asp Val Pro Ser Gly Gly Ile Trp Trp Asp Thr
 35 40 45
 Ile Arg Gln Lys Ile Pro Glu Trp Tyr Asp Ala Gly Ile Ser Ala Ile
 50 55 60
 Trp Ile Pro Pro Ala Ser Lys Gly Met Ser Gly Gly Tyr Ser Met Gly
 65 70 75 80
 Tyr Asp Pro Tyr Asp Tyr Phe Asp Leu Gly Glu Tyr Tyr Gln Lys Gly
 85 90 95
 Thr Val Glu Thr Arg Phe Gly Ser Lys Gln Glu Leu Ile Asn Met Ile
 100 105 110
 Asn Thr Ala His Ala Tyr Gly Ile Lys Val Ile Ala Asp Ile Val Ile
 115 120 125
 Asn His Arg Ala Gly Gly Asp Leu Glu Trp Asn Pro Phe Val Gly Asp
 130 135 140
 Tyr Thr Trp Thr Asp Phe Ser Lys Val Ala Ser Gly Lys Tyr Thr Ala
 145 150 155 160
 Asn Tyr Leu Asp Phe His Pro Asn Glu Leu His Ala Gly Asp Ser Gly
 165 170 175
 Thr Phe Gly Gly Tyr Pro Asp Ile Cys His Asp Lys Ser Trp Asp Gln
 180 185 190
 Tyr Trp Leu Trp Ala Ser Gln Glu Ser Tyr Ala Ala Tyr Leu Arg Ser
 195 200 205
 Ile Gly Ile Asp Ala Trp Arg Phe Asp Tyr Val Lys Gly Tyr Gly Ala
 210 215 220
 Trp Val Val Lys Asp Trp Leu Asn Trp Trp Gly Gly Trp Ala Val Gly
 225 230 235 240
 Glu Tyr Trp Asp Thr Asn Val Asp Ala Leu Leu Asn Trp Ala Tyr Ser
 245 250 255
 Ser Gly Ala Lys Val Phe Asp Phe Pro Leu Tyr Tyr Lys Met Asp Ala
 260 265 270
 Ala Phe Asp Asn Lys Asn Ile Pro Ala Leu Val Glu Ala Leu Lys Asn
 275 280 285
 Gly Gly Thr Val Val Ser Arg Asp Pro Phe Lys Ala Val Thr Phe Val
 290 295 300
 Ala Asn His Asp Thr Asp Ile Ile Trp Asn Lys Tyr Pro Ala Tyr Ala
 305 310 315 320
 Phe Ile Leu Thr Tyr Glu Gly Gln Pro Thr Ile Phe Tyr Arg Asp Tyr
 325 330 335
 Glu Glu Trp Leu Asn Lys Asp Lys Leu Lys Asn Leu Ile Trp Ile His
 340 345 350
 Asp Asn Leu Ala Gly Gly Ser Thr Ser Ile Val Tyr Tyr Asp Ser Asp
 355 360 365
 Glu Met Ile Phe Val Arg Asn Gly Tyr Gly Ser Lys Pro Gly Leu Ile
 370 375 380
 Thr Tyr Ile Asn Leu Gly Ser Ser Lys Val Gly Arg Trp Val Tyr Val
 385 390 395 400

Pro Lys Phe Ala Gly Ala Cys Ile His Glu Tyr Thr Gly Asn Leu Gly
 405 410 415
 Gly Trp Val Asp Lys Tyr Val Tyr Ser Ser Gly Trp Val Tyr Leu Glu
 420 425 430
 Ala Pro Ala Tyr Asp Pro Ala Asn Gly Gln Tyr Gly Tyr Ser Val Trp
 435 440 445
 Ser Tyr Cys Gly Val Gly Ser Glu Lys Asp Glu Leu
 450 455 460

<210> 34
 <211> 825
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 34
 Met Arg Val Leu Leu Val Ala Leu Ala Leu Leu Ala Leu Ala Ala Ser
 1 5 10 15
 Ala Thr Ser Ala Gly His Trp Tyr Lys His Gln Arg Ala Tyr Gln Phe
 20 25 30
 Thr Gly Glu Asp Asp Phe Gly Lys Val Ala Val Val Lys Leu Pro Met
 35 40 45
 Asp Leu Thr Lys Val Gly Ile Ile Val Arg Leu Asn Glu Trp Gln Ala
 50 55 60
 Lys Asp Val Ala Lys Asp Arg Phe Ile Glu Ile Lys Asp Gly Lys Ala
 65 70 75 80
 Glu Val Trp Ile Leu Gln Gly Val Glu Glu Ile Phe Tyr Glu Lys Pro
 85 90 95
 Asp Thr Ser Pro Arg Ile Phe Phe Ala Gln Ala Arg Ser Asn Lys Val
 100 105 110
 Ile Glu Ala Phe Leu Thr Asn Pro Val Asp Thr Lys Lys Lys Glu Leu
 115 120 125
 Phe Lys Val Thr Val Asp Gly Lys Glu Ile Pro Val Ser Arg Val Glu
 130 135 140
 Lys Ala Asp Pro Thr Asp Ile Asp Val Thr Asn Tyr Val Arg Ile Val
 145 150 155 160
 Leu Ser Glu Ser Leu Lys Glu Glu Asp Leu Arg Lys Asp Val Glu Leu
 165 170 175
 Ile Ile Glu Gly Tyr Lys Pro Ala Arg Val Ile Met Met Glu Ile Leu
 180 185 190
 Asp Asp Tyr Tyr Tyr Asp Gly Glu Leu Gly Ala Val Tyr Ser Pro Glu
 195 200 205
 Lys Thr Ile Phe Arg Val Trp Ser Pro Val Ser Lys Trp Val Lys Val
 210 215 220
 Leu Leu Phe Lys Asn Gly Glu Asp Thr Glu Pro Tyr Gln Val Val Asn
 225 230 235 240
 Met Glu Tyr Lys Gly Asn Gly Val Trp Glu Ala Val Val Glu Gly Asp
 245 250 255
 Leu Asp Gly Val Phe Tyr Leu Tyr Gln Leu Glu Asn Tyr Gly Lys Ile
 260 265 270
 Arg Thr Thr Val Asp Pro Tyr Ser Lys Ala Val Tyr Ala Asn Asn Gln
 275 280 285
 Glu Ser Ala Val Val Asn Leu Ala Arg Thr Asn Pro Glu Gly Trp Glu
 290 295 300
 Asn Asp Arg Gly Pro Lys Ile Glu Gly Tyr Glu Asp Ala Ile Ile Tyr

305					310					315				320
Glu	Ile	His	Ile	Ala	Asp	Ile	Thr	Gly	Leu	Glu	Asn	Ser	Gly	Val
				325					330					Lys
Asn	Lys	Gly	Leu	Tyr	Leu	Gly	Leu	Thr	Glu	Glu	Asn	Thr	Lys	Ala
			340					345					350	Pro
Gly	Gly	Val	Thr	Thr	Gly	Leu	Ser	His	Leu	Val	Glu	Leu	Gly	Val
		355					360					365		Thr
His	Val	His	Ile	Leu	Pro	Phe	Phe	Asp	Phe	Tyr	Thr	Gly	Asp	Glu
	370					375					380			Leu
Asp	Lys	Asp	Phe	Glu	Lys	Tyr	Tyr	Asn	Trp	Gly	Tyr	Asp	Pro	Tyr
385					390					395				400
Phe	Met	Val	Pro	Glu	Gly	Arg	Tyr	Ser	Thr	Asp	Pro	Lys	Asn	Pro
				405					410					415
Thr	Arg	Ile	Arg	Glu	Val	Lys	Glu	Met	Val	Lys	Ala	Leu	His	Lys
			420					425					430	His
Gly	Ile	Gly	Val	Ile	Met	Asp	Met	Val	Phe	Pro	His	Thr	Tyr	Gly
	435						440					445		Ile
Gly	Glu	Leu	Ser	Ala	Phe	Asp	Gln	Thr	Val	Pro	Tyr	Tyr	Phe	Tyr
	450					455					460			Arg
Ile	Asp	Lys	Thr	Gly	Ala	Tyr	Leu	Asn	Glu	Ser	Gly	Cys	Gly	Asn
465					470					475				Val
Ile	Ala	Ser	Glu	Arg	Pro	Met	Met	Arg	Lys	Phe	Ile	Val	Asp	Thr
				485					490					Val
Thr	Tyr	Trp	Val	Lys	Glu	Tyr	His	Ile	Asp	Gly	Phe	Arg	Phe	Asp
			500					505					510	Gln
Met	Gly	Leu	Ile	Asp	Lys	Lys	Thr	Met	Leu	Glu	Val	Glu	Arg	Ala
	515						520					525		Leu
His	Lys	Ile	Asp	Pro	Thr	Ile	Ile	Leu	Tyr	Gly	Glu	Pro	Trp	Gly
	530					535					540			Gly
Trp	Gly	Ala	Pro	Ile	Arg	Phe	Gly	Lys	Ser	Asp	Val	Ala	Gly	Thr
545					550					555				His
Val	Ala	Ala	Phe	Asn	Asp	Glu	Phe	Arg	Asp	Ala	Ile	Arg	Gly	Ser
				565					570					Val
Phe	Asn	Pro	Ser	Val	Lys	Gly	Phe	Val	Met	Gly	Gly	Tyr	Gly	Lys
			580					585					590	Glu
Thr	Lys	Ile	Lys	Arg	Gly	Val	Val	Gly	Ser	Ile	Asn	Tyr	Asp	Gly
	595						600					605		Lys
Leu	Ile	Lys	Ser	Phe	Ala	Leu	Asp	Pro	Glu	Glu	Thr	Ile	Asn	Tyr
	610					615					620			Ala
Ala	Cys	His	Asp	Asn	His	Thr	Leu	Trp	Asp	Lys	Asn	Tyr	Leu	Ala
625					630					635				Ala
Lys	Ala	Asp	Lys	Lys	Lys	Glu	Trp	Thr	Glu	Glu	Glu	Leu	Lys	Asn
				645					650					Ala
Gln	Lys	Leu	Ala	Gly	Ala	Ile	Leu	Leu	Ser	Gln	Gly	Val	Pro	Phe
			660					665				670		
Leu	His	Gly	Gly	Gln	Asp	Phe	Cys	Arg	Thr	Thr	Asn	Phe	Asn	Asp
	675						680					685		Asn
Ser	Tyr	Asn	Ala	Pro	Ile	Ser	Ile	Asn	Gly	Phe	Asp	Tyr	Glu	Arg
	690					695					700			Lys
Leu	Gln	Phe	Ile	Asp	Val	Phe	Asn	Tyr	His	Lys	Gly	Leu	Ile	Lys
705					710					715				Leu
Arg	Lys	Glu	His	Pro	Ala	Phe	Arg	Leu	Lys	Asn	Ala	Glu	Glu	Ile
				725					730					Lys
Lys	His	Leu	Glu	Phe	Leu	Pro	Gly	Gly	Arg	Arg	Ile	Val	Ala	Phe
			740					745				750		Met
Leu	Lys	Asp	His	Ala	Gly	Gly	Asp	Pro	Trp	Lys	Asp	Ile	Val	Val
	755						760					765		Ile
Tyr	Asn	Gly	Asn	Leu	Glu	Lys	Thr	Thr	Tyr	Lys	Leu	Pro	Glu	Gly
														Lys

```

      770              775              780
Trp Asn Val Val Val Asn Ser Gln Lys Ala Gly Thr Glu Val Ile Glu
785              790              795              800
Thr Val Glu Gly Thr Ile Glu Leu Asp Pro Leu Ser Ala Tyr Val Leu
      805              810              815
Tyr Arg Glu Ser Glu Lys Asp Glu Leu
      820              825

```

<210> 35
 <211> 460
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

```

<400> 35
Met Arg Val Leu Leu Val Ala Leu Ala Leu Leu Ala Leu Ala Ala Ser
 1              5              10              15
Ala Thr Ser Ala Lys Tyr Leu Glu Leu Glu Gly Gly Val Ile Met
      20              25              30
Gln Ala Phe Tyr Trp Asp Val Pro Ser Gly Gly Ile Trp Trp Asp Thr
      35              40              45
Ile Arg Gln Lys Ile Pro Glu Trp Tyr Asp Ala Gly Ile Ser Ala Ile
      50              55              60
Trp Ile Pro Pro Ala Ser Lys Gly Met Ser Gly Gly Tyr Ser Met Gly
65              70              75              80
Tyr Asp Pro Tyr Asp Tyr Phe Asp Leu Gly Glu Tyr Tyr Gln Lys Gly
      85              90              95
Thr Val Glu Thr Arg Phe Gly Ser Lys Gln Glu Leu Ile Asn Met Ile
      100              105              110
Asn Thr Ala His Ala Tyr Gly Ile Lys Val Ile Ala Asp Ile Val Ile
      115              120              125
Asn His Arg Ala Gly Gly Asp Leu Glu Trp Asn Pro Phe Val Gly Asp
      130              135              140
Tyr Thr Trp Thr Asp Phe Ser Lys Val Ala Ser Gly Lys Tyr Thr Ala
145              150              155              160
Asn Tyr Leu Asp Phe His Pro Asn Glu Leu His Ala Gly Asp Ser Gly
      165              170              175
Thr Phe Gly Gly Tyr Pro Asp Ile Cys His Asp Lys Ser Trp Asp Gln
      180              185              190
Tyr Trp Leu Trp Ala Ser Gln Glu Ser Tyr Ala Ala Tyr Leu Arg Ser
      195              200              205
Ile Gly Ile Asp Ala Trp Arg Phe Asp Tyr Val Lys Gly Tyr Gly Ala
      210              215              220
Trp Val Val Lys Asp Trp Leu Asn Trp Trp Gly Gly Trp Ala Val Gly
225              230              235              240
Glu Tyr Trp Asp Thr Asn Val Asp Ala Leu Leu Asn Trp Ala Tyr Ser
      245              250              255
Ser Gly Ala Lys Val Phe Asp Phe Pro Leu Tyr Tyr Lys Met Asp Ala
      260              265              270
Ala Phe Asp Asn Lys Asn Ile Pro Ala Leu Val Glu Ala Leu Lys Asn
      275              280              285
Gly Gly Thr Val Val Ser Arg Asp Pro Phe Lys Ala Val Thr Phe Val
      290              295              300
Ala Asn His Asp Thr Asp Ile Ile Trp Asn Lys Tyr Pro Ala Tyr Ala
305              310              315              320

```

```

Phe Ile Leu Thr Tyr Glu Gly Gln Pro Thr Ile Phe Tyr Arg Asp Tyr
      325      330      335
Glu Glu Trp Leu Asn Lys Asp Lys Leu Lys Asn Leu Ile Trp Ile His
      340      345      350
Asp Asn Leu Ala Gly Gly Ser Thr Ser Ile Val Tyr Tyr Asp Ser Asp
      355      360      365
Glu Met Ile Phe Val Arg Asn Gly Tyr Gly Ser Lys Pro Gly Leu Ile
      370      375      380
Thr Tyr Ile Asn Leu Gly Ser Ser Lys Val Gly Arg Trp Val Tyr Val
      385      390      395      400
Pro Lys Phe Ala Gly Ala Cys Ile His Glu Tyr Thr Gly Asn Leu Gly
      405      410      415
Gly Trp Val Asp Lys Tyr Val Tyr Ser Ser Gly Trp Val Tyr Leu Glu
      420      425      430
Ala Pro Ala Tyr Asp Pro Ala Asn Gly Gln Tyr Gly Tyr Ser Val Trp
      435      440      445
Ser Tyr Cys Gly Val Gly Ser Glu Lys Asp Glu Leu
      450      455      460

```

<210> 36
 <211> 718
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

```

<400> 36
Met Arg Val Leu Leu Val Ala Leu Ala Leu Leu Ala Leu Ala Ala Ser
  1      5      10      15
Ala Thr Ser Met Glu Thr Ile Lys Ile Tyr Glu Asn Lys Gly Val Tyr
  20      25      30
Lys Val Val Ile Gly Glu Pro Phe Pro Pro Ile Glu Phe Pro Leu Glu
  35      40      45
Gln Lys Ile Ser Ser Asn Lys Ser Leu Ser Glu Leu Gly Leu Thr Ile
  50      55      60
Val Gln Gln Gly Asn Lys Val Ile Val Glu Lys Ser Leu Asp Leu Lys
  65      70      75      80
Glu His Ile Ile Gly Leu Gly Glu Lys Ala Phe Glu Leu Asp Arg Lys
  85      90      95
Arg Lys Arg Tyr Val Met Tyr Asn Val Asp Ala Gly Ala Tyr Lys Lys
  100      105      110
Tyr Gln Asp Pro Leu Tyr Val Ser Ile Pro Leu Phe Ile Ser Val Lys
  115      120      125
Asp Gly Val Ala Thr Gly Tyr Phe Phe Asn Ser Ala Ser Lys Val Ile
  130      135      140
Phe Asp Val Gly Leu Glu Tyr Asp Lys Val Ile Val Thr Ile Pro
  145      150      155      160
Glu Asp Ser Val Glu Phe Tyr Val Ile Glu Gly Pro Arg Ile Glu Asp
  165      170      175
Val Leu Glu Lys Tyr Thr Glu Leu Thr Gly Lys Pro Phe Leu Pro Pro
  180      185      190
Met Trp Ala Phe Gly Tyr Met Ile Ser Arg Tyr Ser Tyr Tyr Pro Gln
  195      200      205
Asp Lys Val Val Glu Leu Val Asp Ile Met Gln Lys Glu Gly Phe Arg
  210      215      220
Val Ala Gly Val Phe Leu Asp Ile His Tyr Met Asp Ser Tyr Lys Leu

```

225					230					235				240
Phe	Thr	Trp	His	Pro	Tyr	Arg	Phe	Pro	Glu	Pro	Lys	Lys	Leu	Ile
				245					250					255
Glu	Leu	His	Lys	Arg	Asn	Val	Lys	Leu	Ile	Thr	Ile	Val	Asp	His
			260					265					270	
Ile	Arg	Val	Asp	Gln	Asn	Tyr	Ser	Pro	Phe	Leu	Ser	Gly	Met	Gly
		275					280				285			Lys
Phe	Cys	Glu	Ile	Glu	Ser	Gly	Glu	Leu	Phe	Val	Gly	Lys	Met	Trp
	290					295				300				Pro
Gly	Thr	Thr	Val	Tyr	Pro	Asp	Phe	Phe	Arg	Glu	Asp	Thr	Arg	Glu
305					310					315				320
Trp	Ala	Gly	Leu	Ile	Ser	Glu	Trp	Leu	Ser	Gln	Gly	Val	Asp	Gly
				325				330						335
Trp	Leu	Asp	Met	Asn	Glu	Pro	Thr	Asp	Phe	Ser	Arg	Ala	Ile	Glu
		340						345					350	Ile
Arg	Asp	Val	Leu	Ser	Ser	Leu	Pro	Val	Gln	Phe	Arg	Asp	Asp	Arg
	355						360					365		Leu
Val	Thr	Thr	Phe	Pro	Asp	Asn	Val	Val	His	Tyr	Leu	Arg	Gly	Lys
	370					375					380			Arg
Val	Lys	His	Glu	Lys	Val	Arg	Asn	Ala	Tyr	Pro	Leu	Tyr	Glu	Ala
385					390					395				400
Ala	Thr	Phe	Lys	Gly	Phe	Arg	Thr	Ser	His	Arg	Asn	Glu	Ile	Phe
				405					410					415
Leu	Ser	Arg	Ala	Gly	Tyr	Ala	Gly	Ile	Gln	Arg	Tyr	Ala	Phe	Ile
			420					425					430	Trp
Thr	Gly	Asp	Asn	Thr	Pro	Ser	Trp	Asp	Asp	Leu	Lys	Leu	Gln	Leu
	435						440				445			Gln
Leu	Val	Leu	Gly	Leu	Ser	Ile	Ser	Gly	Val	Pro	Phe	Val	Gly	Cys
	450					455				460				Asp
Ile	Gly	Gly	Phe	Gln	Gly	Arg	Asn	Phe	Ala	Glu	Ile	Asp	Asn	Ser
465					470					475				480
Asp	Leu	Leu	Val	Lys	Tyr	Tyr	Ala	Leu	Ala	Leu	Phe	Phe	Pro	Phe
				485				490						495
Arg	Ser	His	Lys	Ala	Thr	Asp	Gly	Ile	Asp	Thr	Glu	Pro	Val	Phe
			500					505					510	Leu
Pro	Asp	Tyr	Tyr	Lys	Glu	Lys	Val	Lys	Glu	Ile	Val	Glu	Leu	Arg
	515						520					525		Tyr
Lys	Phe	Leu	Pro	Tyr	Ile	Tyr	Ser	Leu	Ala	Leu	Glu	Ala	Ser	Glu
	530					535				540				Lys
Gly	His	Pro	Val	Ile	Arg	Pro	Leu	Phe	Tyr	Glu	Phe	Gln	Asp	Asp
545					550					555				560
Asp	Met	Tyr	Arg	Ile	Glu	Asp	Glu	Tyr	Met	Val	Gly	Lys	Tyr	Leu
				565				570						575
Tyr	Ala	Pro	Ile	Val	Ser	Lys	Glu	Glu	Ser	Arg	Leu	Val	Thr	Leu
		580						585					590	Pro
Arg	Gly	Lys	Trp	Tyr	Asn	Tyr	Trp	Asn	Gly	Glu	Ile	Ile	Asn	Gly
	595						600					605		Lys
Ser	Val	Val	Lys	Ser	Thr	His	Glu	Leu	Pro	Ile	Tyr	Leu	Arg	Glu
	610					615					620			Gly
Ser	Ile	Ile	Pro	Leu	Glu	Gly	Asp	Glu	Leu	Ile	Val	Tyr	Gly	Glu
625					630					635				640
Ser	Phe	Lys	Arg	Tyr	Asp	Asn	Ala	Glu	Ile	Thr	Ser	Ser	Ser	Asn
				645				650						655
Ile	Lys	Phe	Ser	Arg	Glu	Ile	Tyr	Val	Ser	Lys	Leu	Thr	Ile	Thr
		660						665					670	Ser
Glu	Lys	Pro	Val	Ser	Lys	Ile	Ile	Val	Asp	Asp	Ser	Lys	Glu	Ile
	675						680					685		Gln
Val	Glu	Lys	Thr	Met	Gln	Asn	Thr	Tyr	Val	Ala	Lys	Ile	Asn	Gln
														Lys

690 695 700
 Ile Arg Gly Lys Ile Asn Leu Glu Ser Glu Lys Asp Glu Leu
 705 710 715

<210> 37
 <211> 1434
 <212> DNA
 <213> Thermotoga maritima

<400> 37
 atgaaagaaa ccgctgctgc taaattcgaa cgccagcaca tggacagccc agatctgggt 60
 accctggtgc cagcggttc catggccgag ttcttcccg agatcccga gatccagttc 120
 gagggcaagg agtccacca cccgctcgcc ttccgcttct acgaccgaa cgaggtgatc 180
 gacggcaagc cgctcaagga ccacctcaag ttctccgtgg ccttctggca caccttcgtg 240
 aacgagggcc gcgaccggt cgcgacccg accgccgagc gcccggtgaa ccgcttctcc 300
 gacccgatgg acaaggcctt cgcccgctg gacgccctt tcgagttctg cgagaagctc 360
 aacatcgagt acttctgctt ccacgaccgc gacatcgccc cggagggcaa gaccctccgc 420
 gagaccaaca agatcctcga caaggtggtg gagcgcatca aggagcgcat gaaggactcc 480
 aacgtgaagc tcctctgggg caccgccaac ctcttctccc acccgcgcta catgcacggc 540
 gccgccacca cctgctccgc cgactgttgc gctacgccg ccgccaggt gaagaaggcc 600
 ttggagatca ccaaggagct gggcgggcag ggctacgtgt tctggggcgg ccgcgagggc 660
 tacgagaccc tcctcaacac cgacctcggc ctggagctgg agaacctcgc ccgcttctc 720
 cgcatggccg tggagtacgc caagaagatc ggcttcaccg gccagttcct catcgagccg 780
 aagccgaagg agccgaccaa gcaccagtac gacttcgacg tggccaccgc ctacgccttc 840
 ctcaagaacc acggcctcga cgagtacttc aagttcaaca tcgaggccaa ccacgccacc 900
 ctgcgccggc acaccttcca gcacgagctg cgcatggccc gcatcctcgg caagctcggc 960
 tccatcgacg ccaaccaggg cgacctctc ctcggtggg acaccgacca gttcccggacc 1020
 aacatctacg acaccaccct cgccatgtac gaggtgatca aggccggcg cttcaccagg 1080
 ggcggcctca acttcgacgc caaggtgcgc cgcgcctcct acaaggtgga ggacctcttc 1140
 atcggccaca tcgccggcat ggacaccttc gccctcggct tcaagatcgc ctacaagctc 1200
 gccaaaggac gcgtgttcga caagttcatc gaggagaagt accgctcctt caaggagggc 1260
 atcggaagg agatcggtga gggcaagacc gacttcgaga agctggagga gtacatcatc 1320
 gacaaggagg acatcgagct gccgtccggc aagcaggagt acctggagtc cctcctcaac 1380
 tcctacatcg tgaagaccat cgccgagctg cgctccgaga aggacgagct gtga 1434

<210> 38
 <211> 477
 <212> PRT
 <213> Thermotoga maritima

<400> 38
 Met Lys Glu Thr Ala Ala Ala Lys Phe Glu Arg Gln His Met Asp Ser
 1 5 10 15
 Pro Asp Leu Gly Thr Leu Val Pro Arg Gly Ser Met Ala Glu Phe Phe
 20 25 30
 Pro Glu Ile Pro Lys Ile Gln Phe Glu Gly Lys Glu Ser Thr Asn Pro
 35 40 45
 Leu Ala Phe Arg Phe Tyr Asp Pro Asn Glu Val Ile Asp Gly Lys Pro
 50 55 60
 Leu Lys Asp His Leu Lys Phe Ser Val Ala Phe Trp His Thr Phe Val
 65 70 75 80
 Asn Glu Gly Arg Asp Pro Phe Gly Asp Pro Thr Ala Glu Arg Pro Trp
 85 90 95
 Asn Arg Phe Ser Asp Pro Met Asp Lys Ala Phe Ala Arg Val Asp Ala
 100 105 110
 Leu Phe Glu Phe Cys Glu Lys Leu Asn Ile Glu Tyr Phe Cys Phe His
 115 120 125

Asp Arg Asp Ile Ala Pro Glu Gly Lys Thr Leu Arg Glu Thr Asn Lys
 130 135 140
 Ile Leu Asp Lys Val Val Glu Arg Ile Lys Glu Arg Met Lys Asp Ser
 145 150 155 160
 Asn Val Lys Leu Leu Trp Gly Thr Ala Asn Leu Phe Ser His Pro Arg
 165 170 175
 Tyr Met His Gly Ala Ala Thr Thr Cys Ser Ala Asp Val Phe Ala Tyr
 180 185 190
 Ala Ala Ala Gln Val Lys Lys Ala Leu Glu Ile Thr Lys Glu Leu Gly
 195 200 205
 Gly Glu Gly Tyr Val Phe Trp Gly Gly Arg Glu Gly Tyr Glu Thr Leu
 210 215 220
 Leu Asn Thr Asp Leu Gly Leu Glu Leu Glu Asn Leu Ala Arg Phe Leu
 225 230 235 240
 Arg Met Ala Val Glu Tyr Ala Lys Lys Ile Gly Phe Thr Gly Gln Phe
 245 250 255
 Leu Ile Glu Pro Lys Pro Lys Glu Pro Thr Lys His Gln Tyr Asp Phe
 260 265 270
 Asp Val Ala Thr Ala Tyr Ala Phe Leu Lys Asn His Gly Leu Asp Glu
 275 280 285
 Tyr Phe Lys Phe Asn Ile Glu Ala Asn His Ala Thr Leu Ala Gly His
 290 295 300
 Thr Phe Gln His Glu Leu Arg Met Ala Arg Ile Leu Gly Lys Leu Gly
 305 310 315 320
 Ser Ile Asp Ala Asn Gln Gly Asp Leu Leu Leu Gly Trp Asp Thr Asp
 325 330 335
 Gln Phe Pro Thr Asn Ile Tyr Asp Thr Thr Leu Ala Met Tyr Glu Val
 340 345 350
 Ile Lys Ala Gly Gly Phe Thr Lys Gly Gly Leu Asn Phe Asp Ala Lys
 355 360 365
 Val Arg Arg Ala Ser Tyr Lys Val Glu Asp Leu Phe Ile Gly His Ile
 370 375 380
 Ala Gly Met Asp Thr Phe Ala Leu Gly Phe Lys Ile Ala Tyr Lys Leu
 385 390 395 400
 Ala Lys Asp Gly Val Phe Asp Lys Phe Ile Glu Glu Lys Tyr Arg Ser
 405 410 415
 Phe Lys Glu Gly Ile Gly Lys Glu Ile Val Glu Gly Lys Thr Asp Phe
 420 425 430
 Glu Lys Leu Glu Glu Tyr Ile Ile Asp Lys Glu Asp Ile Glu Leu Pro
 435 440 445
 Ser Gly Lys Gln Glu Tyr Leu Glu Ser Leu Leu Asn Ser Tyr Ile Val
 450 455 460
 Lys Thr Ile Ala Glu Leu Arg Ser Glu Lys Asp Glu Leu
 465 470 475

<210> 39
 <211> 1434
 <212> DNA
 <213> Thermotoga neapolitana

<400> 39
 atgaaagaaa ccgctgctgc taaattcgaa cgccagcaca tggacagccc agatctgggt 60
 accctggtgc cagcggttc catggccgag ttcttcccgg agatcccga ggtgcagttc 120
 gagggcaagg agtccaccaa cccgctcgcc ttcaagttct acgaccgga ggagatcatc 180
 gacggcaagc cgctcaagga ccacctcaag ttctccgtgg ccttctggca caccttcgtg 240
 aacgagggcc gcgacccggt cggcgacccg accgccgacc gcccggtggaa ccgctacacc 300
 gacccgatgg acaaggcctt cgcccgcgtg gacgccctct tcgagttctg cgagaagctc 360

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aacatcgagt acttctgctt ccacgaccgc gacatcgccc cggagggcaa gaccctccgc 420
gagaccaaca agatcctcga caaggtggtg gagcgcatca aggagcgcat gaaggactcc 480
aacgtgaagc tcctctgggg caccgccaac ctcttctccc acccgcgcta catgcacggc 540
gccgccacca cctgctccgc cgacgtgttc gcctacgccg ccgcccaggt gaagaaggcc 600
ctggagatca ccaaggagct gggcgggcag ggctacgtgt tctggggcgg ccgcgagggc 660
tacgagaccc tcctcaacac cgacctcggc ttcgagctgg agaacctcgc ccgcttcctc 720
cgcatggccg tggactacgc caagcgcatc ggcttcaccg gccagttcct catcgagccg 780
aagccgaagc agccgaccac gcaccagtac gacttcgacg tggccaccgc ctacgccttc 840
ctcaagtccc acggcctcga cgagtacttc aagttcaaca tcgaggccaa ccacgccacc 900
ctcgccggcc acaccttcca gcacgagctg cgcattggccc gcatcctcgg caagctcggc 960
tccatcgacg ccaaccaggg cgacctcctc ctcggtggg acaccgacca gttcccgcacc 1020
aacgtgtacg acaccacctt cgccatgtac gaggtgatca aggccggcgg cttcaccaag 1080
ggcgccctca acttcgacgc caaggtgcgc cgcgcctcct acaagggtga ggacctcttc 1140
atcgccaca tcgcccgcac ggacaccttc gccctcggct tcaagggtgc ctacaagctc 1200
gtgaaggacg gcgtgctcga caagttcatc gaggagaagt accgctcctt ccgcgagggc 1260
atcgcccgcg acatcgtgga gggcaagggt gacttcgaga agctggagga gtacatcatc 1320
gacaaggaga ccatcgagct gccgtccggc aagcaggagt acctggagtc cctcatcaac 1380
tctacatcg tgaagaccat cctggagctg cgctccgaga aggacgagct gtga 1434

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<210> 40
 <211> 477
 <212> PRT
 <213> Thermotoga neapolitana

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<400> 40
Met Lys Glu Thr Ala Ala Lys Phe Glu Arg Gln His Met Asp Ser
 1      5      10      15
Pro Asp Leu Gly Thr Leu Val Pro Arg Gly Ser Met Ala Glu Phe Phe
      20      25      30
Pro Glu Ile Pro Lys Val Gln Phe Glu Gly Lys Glu Ser Thr Asn Pro
      35      40      45
Leu Ala Phe Lys Phe Tyr Asp Pro Glu Glu Ile Ile Asp Gly Lys Pro
      50      55      60
Leu Lys Asp His Leu Lys Phe Ser Val Ala Phe Trp His Thr Phe Val
      65      70      75      80
Asn Glu Gly Arg Asp Pro Phe Gly Asp Pro Thr Ala Asp Arg Pro Trp
      85      90      95
Asn Arg Tyr Thr Asp Pro Met Asp Lys Ala Phe Ala Arg Val Asp Ala
      100      105      110
Leu Phe Glu Phe Cys Glu Lys Leu Asn Ile Glu Tyr Phe Cys Phe His
      115      120      125
Asp Arg Asp Ile Ala Pro Glu Gly Lys Thr Leu Arg Glu Thr Asn Lys
      130      135      140
Ile Leu Asp Lys Val Val Glu Arg Ile Lys Glu Arg Met Lys Asp Ser
      145      150      155      160
Asn Val Lys Leu Leu Trp Gly Thr Ala Asn Leu Phe Ser His Pro Arg
      165      170      175
Tyr Met His Gly Ala Ala Thr Thr Cys Ser Ala Asp Val Phe Ala Tyr
      180      185      190
Ala Ala Ala Gln Val Lys Lys Ala Leu Glu Ile Thr Lys Glu Leu Gly
      195      200      205
Gly Glu Gly Tyr Val Phe Trp Gly Gly Arg Glu Gly Tyr Glu Thr Leu
      210      215      220
Leu Asn Thr Asp Leu Gly Phe Glu Leu Glu Asn Leu Ala Arg Phe Leu
      225      230      235      240
Arg Met Ala Val Asp Tyr Ala Lys Arg Ile Gly Phe Thr Gly Gln Phe
      245      250      255
Leu Ile Glu Pro Lys Pro Lys Glu Pro Thr Lys His Gln Tyr Asp Phe

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260 265 270
 Asp Val Ala Thr Ala Tyr Ala Phe Leu Lys Ser His Gly Leu Asp Glu
 275 280 285
 Tyr Phe Lys Phe Asn Ile Glu Ala Asn His Ala Thr Leu Ala Gly His
 290 295 300
 Thr Phe Gln His Glu Leu Arg Met Ala Arg Ile Leu Gly Lys Leu Gly
 305 310 315 320
 Ser Ile Asp Ala Asn Gln Gly Asp Leu Leu Leu Gly Trp Asp Thr Asp
 325 330 335
 Gln Phe Pro Thr Asn Val Tyr Asp Thr Thr Leu Ala Met Tyr Glu Val
 340 345 350
 Ile Lys Ala Gly Gly Phe Thr Lys Gly Gly Leu Asn Phe Asp Ala Lys
 355 360 365
 Val Arg Arg Ala Ser Tyr Lys Val Glu Asp Leu Phe Ile Gly His Ile
 370 375 380
 Ala Gly Met Asp Thr Phe Ala Leu Gly Phe Lys Val Ala Tyr Lys Leu
 385 390 395 400
 Val Lys Asp Gly Val Leu Asp Lys Phe Ile Glu Glu Lys Tyr Arg Ser
 405 410 415
 Phe Arg Glu Gly Ile Gly Arg Asp Ile Val Glu Gly Lys Val Asp Phe
 420 425 430
 Glu Lys Leu Glu Glu Tyr Ile Ile Asp Lys Glu Thr Ile Glu Leu Pro
 435 440 445
 Ser Gly Lys Gln Glu Tyr Leu Glu Ser Leu Ile Asn Ser Tyr Ile Val
 450 455 460
 Lys Thr Ile Leu Glu Leu Arg Ser Glu Lys Asp Glu Leu
 465 470 475

<210> 41
 <211> 1435
 <212> DNA
 <213> Thermotoga maritima

<400> 41
 atgggcagca gccatcatca tcatcatcac agcagcggcc tgggtgccgcg cggcagccat 60
 atggctagca tgactgggtg acagcaaatg ggctcggatcc ccattggccga gttcttccc 120
 gagatcccga agatccagtt cgaggggcaag gattccacca acccgctcgc cttccgcttc 180
 tacgaccgga acgagggtgat cgacgggcaag ccgctcaagg accacctcaa gttctccgtg 240
 gccttctggc acaccttcgt gaacgagggc cgcgaccgt tggcgaccc gaccgcccag 300
 cgcccgtgga accgcttctc cgaccgatg gacaaggcct tggccgcgt ggacgccctc 360
 ttcgagttct gcgagaagct caacatcgag tactttctgt tccacgaccg cgacatcccc 420
 cggagggcaa gacctccgc gagaccaaca agatcctcga caaggtgggt gagcgcatca 480
 aggagcgcac gaaggactcc aacgtgaagc tctctgggg caccgccaac ctcttctccc 540
 acccgcgcta catgcacggc gccgccacca cctgctccgc cgacgtgttc gcctacgccg 600
 ccgcccaggt gaagaaggcc ctggagatca ccaaggagct gggcggcgag ggctacgtgt 660
 tctggggcgg ccgcgagggc tacgagaccc tctcaaacac cgacctcggc ctggagctgg 720
 agaacctcgc ccgcttctc cgcatggccg tggagtacgc caagaagatc ggcttcaccg 780
 gccagttcct catcgagccg aagccgaagg agccgaocaa gcaccagtac gcttcgacgt 840
 ggccaccgcc tacgccttcc tcaagaacca cggcctcgac gactacttca agttcaacat 900
 cgaggccaac cacgccaccc tcgcccggcca cacttccag caccagctgc gcatggccc 960
 catcctcggc aagctcggct ccacgcacgc caaccagggc gacctctcc tcggctggga 1020
 caccgaccag ttcccgaacca acatctacga caccacctc gccatgtacg aggtgatcaa 1080
 ggccggcggc ttcaccaagg gcggcctcaa ctccgacgcc aaggtgcgcc gcgcctcta 1140
 caaggtggag gacctcttca tcggccacat cgcggcatg gacaccttcg cctcggctt 1200
 caagatcgcc tacaagctcg ccaaggacgg cgtgttcgac aagttcatcg aggagaagta 1260
 ccgctccttc aaggagggca tcggcaagga gatcgtggag ggcaagaccg acttcgagaa 1320
 gctggaggag tacatcatcg acaaggagga catcgagctg ccgtccggca agcaggagta 1380

cctggagctcc ctctctcaact cctacatcgt gaagaccatc gccgagctgc gctga

1435

<210> 42
 <211> 478
 <212> PRT
 <213> Thermotoga maritima

<400> 42
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 Arg Gly Ser His Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg
 20 25 30
 Ile Pro Met Ala Glu Phe Phe Pro Glu Ile Pro Lys Ile Gln Phe Glu
 35 40 45
 Gly Lys Glu Ser Thr Asn Pro Leu Ala Phe Arg Phe Tyr Asp Pro Asn
 50 55 60
 Glu Val Ile Asp Gly Lys Pro Leu Lys Asp His Leu Lys Phe Ser Val
 65 70 75 80
 Ala Phe Trp His Thr Phe Val Asn Glu Gly Arg Asp Pro Phe Gly Asp
 85 90 95
 Pro Thr Ala Glu Arg Pro Trp Asn Arg Phe Ser Asp Pro Met Asp Lys
 100 105 110
 Ala Phe Ala Arg Val Asp Ala Leu Phe Glu Phe Cys Glu Lys Leu Asn
 115 120 125
 Ile Glu Tyr Phe Cys Phe His Asp Arg Asp Ile Ala Pro Glu Gly Lys
 130 135 140
 Thr Leu Arg Glu Thr Asn Lys Ile Leu Asp Lys Val Val Glu Arg Ile
 145 150 155 160
 Lys Glu Arg Met Lys Asp Ser Asn Val Lys Leu Leu Trp Gly Thr Ala
 165 170 175
 Asn Leu Phe Ser His Pro Arg Tyr Met His Gly Ala Ala Thr Thr Cys
 180 185 190
 Ser Ala Asp Val Phe Ala Tyr Ala Ala Ala Gln Val Lys Lys Ala Leu
 195 200 205
 Glu Ile Thr Lys Glu Leu Gly Gly Glu Gly Tyr Val Phe Trp Gly Gly
 210 215 220
 Arg Glu Gly Tyr Glu Thr Leu Leu Asn Thr Asp Leu Gly Leu Glu Leu
 225 230 235 240
 Glu Asn Leu Ala Arg Phe Leu Arg Met Ala Val Glu Tyr Ala Lys Lys
 245 250 255
 Ile Gly Phe Thr Gly Gln Phe Leu Ile Glu Pro Lys Pro Lys Glu Pro
 260 265 270
 Thr Lys His Gln Tyr Asp Phe Asp Val Ala Thr Ala Tyr Ala Phe Leu
 275 280 285
 Lys Asn His Gly Leu Asp Glu Tyr Phe Lys Phe Asn Ile Glu Ala Asn
 290 295 300
 His Ala Thr Leu Ala Gly His Thr Phe Gln His Glu Leu Arg Met Ala
 305 310 315 320
 Arg Ile Leu Gly Lys Leu Gly Ser Ile Asp Ala Asn Gln Gly Asp Leu
 325 330 335
 Leu Leu Gly Trp Asp Thr Asp Gln Phe Pro Thr Asn Ile Tyr Asp Thr
 340 345 350
 Thr Leu Ala Met Tyr Glu Val Ile Lys Ala Gly Gly Phe Thr Lys Gly
 355 360 365
 Gly Leu Asn Phe Asp Ala Lys Val Arg Arg Ala Ser Tyr Lys Val Glu
 370 375 380
 Asp Leu Phe Ile Gly His Ile Ala Gly Met Asp Thr Phe Ala Leu Gly
 385 390 395 400

Phe Lys Ile Ala Tyr Lys Leu Ala Lys Asp Gly Val Phe Asp Lys Phe
 405 410 415
 Ile Glu Glu Lys Tyr Arg Ser Phe Lys Glu Gly Ile Gly Lys Glu Ile
 420 425 430
 Val Glu Gly Lys Thr Asp Phe Glu Lys Leu Glu Glu Tyr Ile Ile Asp
 435 440 445
 Lys Glu Asp Ile Glu Leu Pro Ser Gly Lys Gln Glu Tyr Leu Glu Ser
 450 455 460
 Leu Leu Asn Ser Tyr Ile Val Lys Thr Ile Ala Glu Leu Arg
 465 470 475

<210> 43
 <211> 1436
 <212> DNA
 <213> Thermotoga neapolitana

<400> 43
 atgggcagca gccatcatca tcatcatcac agcagcggcc tgggtgccgcg cggcagccat 60
 atggctagca tgactggtgg acagcaaattg ggtcggatcc ccatggccga gttcttccc 120
 gagatcccga aggtgcagtt cgagggcaag gaggccacca acccgctcgc cttcaagttc 180
 tacgaccccg aggagatcat cgacggcaag ccgctcaagg accacctcaa gttctccgtg 240
 gccttctggc acaccttcgt gaacgagggc cgcgaccgt tcggcgaccc gaccgcccac 300
 cgcgcgtgga accgctacac cgacccgatg gacaaggcct tcgcccgcgt ggacgcccctc 360
 ttcgagttct gcgagaagct caacatcgag tacttctgct tccacgaccg cgacatcccc 420
 cggagggcaa gacctccgc gagaccaaca agatcctcga caaggtggtg gagcgcata 480
 aggagcgcat gaaggactcc aacgtgaagc tcctctgggg caccgccaac ctcttctccc 540
 acccgcgcta catgcacggc gccgccacca cctgctccgc cgacgtgttc gcctacgccg 600
 ccgcccaggt gaagaaggcc ctggagatca ccaaggagct gggcggcgag ggctacgtgt 660
 tctggggcgg ccgcgagggc tacgagacc tcctcaaac cgacctcggc ttcgagctgg 720
 agaacctcgc ccgcttcctc cgcattggccg tggactacgc caagcgcata ggcttcaccg 780
 gccagttcct catcgagccg aagccgaagg agccgaccaa gcaccagtag gacttcgacg 840
 tggccaccgc ctacgccttc ctcaagtccc acggcctcga cgagtacttc aagttcaaca 900
 tcgaggccaa ccacgccacc ctgcgcggcc acaccttcca gcacgagctg cgcattggcc 960
 gcattctcgg caagctcggc tccatcgacg ccaaccaggg cgacctcctc ctcggtggg 1020
 acaccgacca gttcccgacc aacgtgtacg acaccacct cgccatgtac gagggtgatca 1080
 aggccggcgg cttcaccaaag ggcggcctca acttcgacgc caaggtgcgc cgcgcctcct 1140
 acaaggtgga ggacctcttc atcgccaca tcgcggcat ggacaccttc gccctcggct 1200
 tcaaggtggc ctacaagctc gtgaaggacg cgtgtctcga caagttcatc gaggagaagt 1260
 accgctcctt ccgcgagggc atcgcccgcg acatcgtgga gggcaagggt gacttcgaga 1320
 agctggagga gtacatcatc gacaaggaga ccatcgagct gccgtccggc aagcaggagt 1380
 acctggagtc cctcatcaac tcctacatcg tgaagaccat cctggagctg cgctga 1436

<210> 44
 <211> 478
 <212> PRT
 <213> Thermotoga neapolitana

<400> 44
 Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro
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 Arg Gly Ser His Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg
 20 25 30
 Ile Pro Met Ala Glu Phe Phe Pro Glu Ile Pro Lys Val Gln Phe Glu
 35 40 45
 Gly Lys Glu Ser Thr Asn Pro Leu Ala Phe Lys Phe Tyr Asp Pro Glu
 50 55 60
 Glu Ile Ile Asp Gly Lys Pro Leu Lys Asp His Leu Lys Phe Ser Val

65	Ala	Phe	Trp	His	Thr	70	Phe	Val	Asn	Glu	Gly	75	Arg	Asp	Pro	Phe	Gly	80	Asp
					85						90						95		
	Pro	Thr	Ala	Asp	Arg	Pro	Trp	Asn	Arg	Tyr	Thr	Asp	Pro	Met	Asp	Lys			
			100						105							110			
	Ala	Phe	Ala	Arg	Val	Asp	Ala	Leu	Phe	Glu	Phe	Cys	Glu	Lys	Leu	Asn			
			115					120					125						
	Ile	Glu	Tyr	Phe	Cys	Phe	His	Asp	Arg	Asp	Ile	Ala	Pro	Glu	Gly	Lys			
		130					135					140							
	Thr	Leu	Arg	Glu	Thr	Asn	Lys	Ile	Leu	Asp	Lys	Val	Val	Glu	Arg	Ile			
		145				150					155					160			
	Lys	Glu	Arg	Met	Lys	Asp	Ser	Asn	Val	Lys	Leu	Leu	Trp	Gly	Thr	Ala			
				165						170						175			
	Asn	Leu	Phe	Ser	His	Pro	Arg	Tyr	Met	His	Gly	Ala	Ala	Thr	Thr	Cys			
			180						185					190					
	Ser	Ala	Asp	Val	Phe	Ala	Tyr	Ala	Ala	Ala	Gln	Val	Lys	Lys	Ala	Leu			
			195					200					205						
	Glu	Ile	Thr	Lys	Glu	Leu	Gly	Gly	Glu	Gly	Tyr	Val	Phe	Trp	Gly	Gly			
		210					215					220							
	Arg	Glu	Gly	Tyr	Glu	Thr	Leu	Leu	Asn	Thr	Asp	Leu	Gly	Phe	Glu	Leu			
		225				230					235					240			
	Glu	Asn	Leu	Ala	Arg	Phe	Leu	Arg	Met	Ala	Val	Asp	Tyr	Ala	Lys	Arg			
				245						250					255				
	Ile	Gly	Phe	Thr	Gly	Gln	Phe	Leu	Ile	Glu	Pro	Lys	Pro	Lys	Glu	Pro			
			260						265					270					
	Thr	Lys	His	Gln	Tyr	Asp	Phe	Asp	Val	Ala	Thr	Ala	Tyr	Ala	Phe	Leu			
			275					280					285						
	Lys	Ser	His	Gly	Leu	Asp	Glu	Tyr	Phe	Lys	Phe	Asn	Ile	Glu	Ala	Asn			
		290					295					300							
	His	Ala	Thr	Leu	Ala	Gly	His	Thr	Phe	Gln	His	Glu	Leu	Arg	Met	Ala			
					310						315					320			
	Arg	Ile	Leu	Gly	Lys	Leu	Gly	Ser	Ile	Asp	Ala	Asn	Gln	Gly	Asp	Leu			
				325						330					335				
	Leu	Leu	Gly	Trp	Asp	Thr	Asp	Gln	Phe	Pro	Thr	Asn	Val	Tyr	Asp	Thr			
			340						345					350					
	Thr	Leu	Ala	Met	Tyr	Glu	Val	Ile	Lys	Ala	Gly	Gly	Phe	Thr	Lys	Gly			
			355					360					365						
	Gly	Leu	Asn	Phe	Asp	Ala	Lys	Val	Arg	Arg	Ala	Ser	Tyr	Lys	Val	Glu			
			370				375					380							
	Asp	Leu	Phe	Ile	Gly	His	Ile	Ala	Gly	Met	Asp	Thr	Phe	Ala	Leu	Gly			
					390						395					400			
	Phe	Lys	Val	Ala	Tyr	Lys	Leu	Val	Lys	Asp	Gly	Val	Leu	Asp	Lys	Phe			
				405						410					415				
	Ile	Glu	Glu	Lys	Tyr	Arg	Ser	Phe	Arg	Glu	Gly	Ile	Gly	Arg	Asp	Ile			
				420					425					430					
	Val	Glu	Gly	Lys	Val	Asp	Phe	Glu	Lys	Leu	Glu	Glu	Tyr	Ile	Ile	Asp			
			435					440					445						
	Lys	Glu	Thr	Ile	Glu	Leu	Pro	Ser	Gly	Lys	Gln	Glu	Tyr	Leu	Glu	Ser			
			450				455					460							
	Leu	Ile	Asn	Ser	Tyr	Ile	Val	Lys	Thr	Ile	Leu	Glu	Leu	Arg					
					470						475								
	465																		

<210> 45
 <211> 1095
 <212> PRT
 <213> Aspergillus shirousami

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<400> 45
Ala Thr Pro Ala Asp Trp Arg Ser Gln Ser Ile Tyr Phe Leu Leu Thr
1      5      10      15
Asp Arg Phe Ala Arg Thr Asp Gly Ser Thr Thr Ala Thr Cys Asn Thr
20      25      30
Ala Asp Gln Lys Tyr Cys Gly Gly Thr Trp Gln Gly Ile Ile Asp Lys
35      40      45
Leu Asp Tyr Ile Gln Gly Met Gly Phe Thr Ala Ile Trp Ile Thr Pro
50      55      60
Val Thr Ala Gln Leu Pro Gln Thr Thr Ala Tyr Gly Asp Ala Tyr His
65      70      75
Gly Tyr Trp Gln Gln Asp Ile Tyr Ser Leu Asn Glu Asn Tyr Gly Thr
85      90      95
Ala Asp Asp Leu Lys Ala Leu Ser Ser Ala Leu His Glu Arg Gly Met
100     105     110
Tyr Leu Met Val Asp Val Val Ala Asn His Met Gly Tyr Asp Gly Ala
115     120     125
Gly Ser Ser Val Asp Tyr Ser Val Phe Lys Pro Phe Ser Ser Gln Asp
130     135     140
Tyr Phe His Pro Phe Cys Phe Ile Gln Asn Tyr Glu Asp Gln Thr Gln
145     150     155
Val Glu Asp Cys Trp Leu Gly Asp Asn Thr Val Ser Leu Pro Asp Leu
165     170     175
Asp Thr Thr Lys Asp Val Val Lys Asn Glu Trp Tyr Asp Trp Val Gly
180     185     190
Ser Leu Val Ser Asn Tyr Ser Ile Asp Gly Leu Arg Ile Asp Thr Val
195     200     205
Lys His Val Gln Lys Asp Phe Trp Pro Gly Tyr Asn Lys Ala Ala Gly
210     215     220
Val Tyr Cys Ile Gly Glu Val Leu Asp Val Asp Pro Ala Tyr Thr Cys
225     230     235
Pro Tyr Gln Asn Val Met Asp Gly Val Leu Asn Tyr Pro Ile Tyr Tyr
245     250     255
Pro Leu Leu Asn Ala Phe Lys Ser Thr Ser Gly Ser Met Asp Asp Leu
260     265     270
Tyr Asn Met Ile Asn Thr Val Lys Ser Asp Cys Pro Asp Ser Thr Leu
275     280     285
Leu Gly Thr Phe Val Glu Asn His Asp Asn Pro Arg Phe Ala Ser Tyr
290     295     300
Thr Asn Asp Ile Ala Leu Ala Lys Asn Val Ala Ala Phe Ile Ile Leu
305     310     315
Asn Asp Gly Ile Pro Ile Ile Tyr Ala Gly Gln Glu Gln His Tyr Ala
325     330     335
Gly Gly Asn Asp Pro Ala Asn Arg Glu Ala Thr Trp Leu Ser Gly Tyr
340     345     350
Pro Thr Asp Ser Glu Leu Tyr Lys Leu Ile Ala Ser Ala Asn Ala Ile
355     360     365
Arg Asn Tyr Ala Ile Ser Lys Asp Thr Gly Phe Val Thr Tyr Lys Asn
370     375     380
Trp Pro Ile Tyr Lys Asp Asp Thr Thr Ile Ala Met Arg Lys Gly Thr
385     390     395
Asp Gly Ser Gln Ile Val Thr Ile Leu Ser Asn Lys Gly Ala Ser Gly
405     410     415
Asp Ser Tyr Thr Leu Ser Leu Ser Gly Ala Gly Tyr Thr Ala Gly Gln
420     425     430
Gln Leu Thr Glu Val Ile Gly Cys Thr Thr Val Thr Val Gly Ser Asp
435     440     445
Gly Asn Val Pro Val Pro Met Ala Gly Gly Leu Pro Arg Val Leu Tyr

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450	Pro	Thr	Glu	Lys	Leu	Ala	Gly	Ser	Lys	Ile	Cys	Ser	Ser	Ser	Lys	Pro
465	Ala	Thr	Leu	Asp	Ser	Trp	Leu	Ser	Asn	Glu	Ala	Thr	Val	Ala	Arg	Thr
					485					490						495
	Ala	Ile	Leu	Asn	Asn	Ile	Gly	Ala	Asp	Gly	Ala	Trp	Val	Ser	Gly	Ala
				500					505					510		
	Asp	Ser	Gly	Ile	Val	Val	Ala	Ser	Pro	Ser	Thr	Asp	Asn	Pro	Asp	Tyr
			515					520					525			
	Phe	Tyr	Thr	Trp	Thr	Arg	Asp	Ser	Gly	Ile	Val	Leu	Lys	Thr	Leu	Val
		530					535					540				
	Asp	Leu	Phe	Arg	Asn	Gly	Asp	Thr	Asp	Leu	Leu	Ser	Thr	Ile	Glu	His
545					550						555					560
	Tyr	Ile	Ser	Ser	Gln	Ala	Ile	Ile	Gln	Gly	Val	Ser	Asn	Pro	Ser	Gly
					565					570						575
	Asp	Leu	Ser	Ser	Gly	Gly	Leu	Gly	Glu	Pro	Lys	Phe	Asn	Val	Asp	Glu
				580					585					590		
	Thr	Ala	Tyr	Ala	Gly	Ser	Trp	Gly	Arg	Pro	Gln	Arg	Asp	Gly	Pro	Ala
		595						600					605			
	Leu	Arg	Ala	Thr	Ala	Met	Ile	Gly	Phe	Gly	Gln	Trp	Leu	Leu	Asp	Asn
		610				615						620				
	Gly	Tyr	Thr	Ser	Ala	Ala	Thr	Glu	Ile	Val	Trp	Pro	Leu	Val	Arg	Asn
625					630						635					640
	Asp	Leu	Ser	Tyr	Val	Ala	Gln	Tyr	Trp	Asn	Gln	Thr	Gly	Tyr	Asp	Leu
				645						650					655	
	Trp	Glu	Glu	Val	Asn	Gly	Ser	Ser	Phe	Phe	Thr	Ile	Ala	Val	Gln	His
				660					665					670		
	Arg	Ala	Leu	Val	Glu	Gly	Ser	Ala	Phe	Ala	Thr	Ala	Val	Gly	Ser	Ser
		675						680					685			
	Cys	Ser	Trp	Cys	Asp	Ser	Gln	Ala	Pro	Gln	Ile	Leu	Cys	Tyr	Leu	Gln
		690				695						700				
	Ser	Phe	Trp	Thr	Gly	Ser	Tyr	Ile	Leu	Ala	Asn	Phe	Asp	Ser	Ser	Arg
705					710						715					720
	Ser	Gly	Lys	Asp	Thr	Asn	Thr	Leu	Leu	Gly	Ser	Ile	His	Thr	Phe	Asp
				725						730					735	
	Pro	Glu	Ala	Gly	Cys	Asp	Asp	Ser	Thr	Phe	Gln	Pro	Cys	Ser	Pro	Arg
				740					745					750		
	Ala	Leu	Ala	Asn	His	Lys	Glu	Val	Val	Asp	Ser	Phe	Arg	Ser	Ile	Tyr
		755						760					765			
	Thr	Leu	Asn	Asp	Gly	Leu	Ser	Asp	Ser	Glu	Ala	Val	Ala	Val	Gly	Arg
		770					775					780				
	Tyr	Pro	Glu	Asp	Ser	Tyr	Tyr	Asn	Gly	Asn	Pro	Trp	Phe	Leu	Cys	Thr
785					790						795					800
	Leu	Ala	Ala	Ala	Glu	Gln	Leu	Tyr	Asp	Ala	Leu	Tyr	Gln	Trp	Asp	Lys
				805						810					815	
	Gln	Gly	Ser	Leu	Glu	Ile	Thr	Asp	Val	Ser	Leu	Asp	Phe	Phe	Lys	Ala
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	Ser	Ile	Val	Glu	Thr	His	Ala	Ala	Ser	Asn	Gly	Ser	Leu	Ser	Glu	Gln
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	Phe	Asp	Lys	Ser	Asp	Gly	Asp	Glu	Leu	Ser	Ala	Arg	Asp	Leu	Thr	Trp
				885					890						895	
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			900					905						910		
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	995	1000
Asn Ile Tyr Leu Val Gly Ser Ile Ser Gln Leu Gly Asp Trp Glu Thr		
	1010	1015
Ser Asp Gly Ile Ala Leu Ser Ala Asp Lys Tyr Thr Ser Ser Asn Pro		
1025	1030	1035
Pro Trp Tyr Val Thr Val Thr Leu Pro Ala Gly Glu Ser Phe Glu Tyr		
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Lys Phe Ile Arg Val Glu Ser Asp Asp Ser Val Glu Trp Glu Ser Asp		
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<210> 46

<211> 3285

<212> DNA

<213> *Aspergillus shirousami*

<400> 46

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<210> 47

<211> 679

<212> PRT

<213> Thermoanaerobacterium thermosaccharolyticum

<400> 47

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20      25      30
Ala Ser Ala Gln Lys Gln Gly Val Gly Thr Ala Asn Asn Tyr Val Ser
35      40      45
Arg Val Trp Phe Thr Leu Ala Asn Gly Ala Ile Ser Glu Val Tyr Tyr
50      55      60
Pro Thr Ile Asp Thr Ala Asp Val Lys Glu Ile Lys Phe Ile Val Thr
65      70      75      80
Asp Gly Lys Ser Phe Val Ser Asp Glu Thr Lys Asp Ala Ile Ser Lys
85      90      95
Val Glu Lys Phe Thr Asp Lys Ser Leu Gly Tyr Lys Leu Val Asn Thr
100     105     110
Asp Lys Lys Gly Arg Tyr Arg Ile Thr Lys Glu Ile Phe Thr Asp Val
115     120     125
Lys Arg Asn Ser Leu Ile Met Lys Ala Lys Phe Glu Ala Leu Glu Gly
130     135     140
Ser Ile His Asp Tyr Lys Leu Tyr Leu Ala Tyr Asp Pro His Ile Lys
145     150     155     160
Asn Gln Gly Ser Tyr Asn Glu Gly Tyr Val Ile Lys Ala Asn Asn Asn
165     170     175
Glu Met Leu Met Ala Lys Arg Asp Asn Val Tyr Thr Ala Leu Ser Ser

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645
 Ala Glu Tyr Val Ile Leu Phe Ala Ser Asn Ile Glu His Lys Val Leu
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 Asp Met Pro Asp Ile Val Tyr
 675

<210> 48
 <211> 2037
 <212> DNA
 <213> Thermoanaerobacterium thermosaccharolyticum

<220>
 <223> synthetic

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<210> 49
 <211> 579
 <212> PRT
 <213> Rhizopus oryzae

<400> 49
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Ser Lys Lys Val	Thr Val Ile Tyr	Ala Asp Gly Ser	Asp Asn Trp Asn
35	40	45	
Asn Asn Gly Asn	Thr Ile Ala Ala	Ser Tyr Ser Ala	Pro Ile Ser Gly
50	55	60	
Ser Asn Tyr Glu	Tyr Trp Thr Phe	Ser Ala Ser Ile	Asn Gly Ile Lys
65	70	75	80
Glu Phe Tyr Ile	Lys Tyr Glu Val	Ser Gly Lys Thr	Tyr Tyr Asp Asn
85	90	95	
Asn Asn Ser Ala	Asn Tyr Gln Val	Ser Thr Ser Lys	Pro Thr Thr Thr
100	105	110	
Thr Ala Thr Ala	Thr Thr Thr Thr	Ala Pro Ser Thr	Ser Thr Thr Thr
115	120	125	
Pro Pro Ser Arg	Ser Glu Pro Ala	Thr Phe Pro Thr	Gly Asn Ser Thr
130	135	140	
Ile Ser Ser Trp	Ile Lys Lys Gln	Glu Gly Ile Ser	Arg Phe Ala Met
145	150	155	160
Leu Arg Asn Ile	Asn Pro Pro Gly	Ser Ala Thr Gly	Phe Ile Ala Ala
165	170	175	
Ser Leu Ser Thr	Ala Gly Pro Asp	Tyr Tyr Tyr Ala	Trp Thr Arg Asp
180	185	190	
Ala Ala Leu Thr	Ser Asn Val Ile	Val Tyr Glu Tyr	Asn Thr Thr Leu
195	200	205	
Ser Gly Asn Lys	Thr Ile Leu Asn	Val Leu Lys Asp	Tyr Val Thr Phe
210	215	220	
Ser Val Lys Thr	Gln Ser Thr Ser	Thr Val Cys Asn	Cys Leu Gly Glu
225	230	235	240
Pro Lys Phe Asn	Pro Asp Ala Ser	Gly Tyr Thr Gly	Ala Trp Gly Arg
245	250	255	
Pro Gln Asn Asp	Gly Pro Ala Glu	Arg Ala Thr Thr	Phe Ile Leu Phe
260	265	270	
Ala Asp Ser Tyr	Leu Thr Gln Thr	Lys Asp Ala Ser	Tyr Val Thr Gly
275	280	285	
Thr Leu Lys Pro	Ala Ile Phe Lys	Asp Leu Asp Tyr	Val Val Asn Val
290	295	300	
Trp Ser Asn Gly	Cys Phe Asp Leu	Trp Glu Glu Val	Asn Gly Val His
305	310	315	320
Phe Tyr Thr Leu	Met Val Met Arg	Lys Gly Leu Leu	Leu Gly Ala Asp
325	330	335	
Phe Ala Lys Arg	Asn Gly Asp Ser	Thr Arg Ala Ser	Thr Tyr Ser Ser
340	345	350	
Thr Ala Ser Thr	Ile Ala Asn Lys	Ile Ser Ser Phe	Trp Val Ser Ser
355	360	365	
Asn Asn Trp Ile	Gln Val Ser Gln	Ser Val Thr Gly	Gly Val Ser Lys
370	375	380	
Lys Gly Leu Asp	Val Ser Thr Leu	Leu Ala Ala Asn	Leu Gly Ser Val
385	390	395	400
Asp Asp Gly Phe	Phe Thr Pro Gly	Ser Glu Lys Ile	Leu Ala Thr Ala
405	410	415	
Val Ala Val Glu	Asp Ser Phe Ala	Ser Leu Tyr Pro	Ile Asn Lys Asn
420	425	430	
Leu Pro Ser Tyr	Leu Gly Asn Ser	Ile Gly Arg Tyr	Pro Glu Asp Thr
435	440	445	
Tyr Asn Gly Asn	Gly Asn Ser Gln	Gly Asn Ser Trp	Phe Leu Ala Val
450	455	460	
Thr Gly Tyr Ala	Glu Leu Tyr Tyr	Arg Ala Ile Lys	Glu Trp Ile Gly

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Asn Gly Gly Val Thr Val Ser Ser Ile Ser Leu Pro Phe Phe Lys Lys
          485          490          495
Phe Asp Ser Ser Ala Thr Ser Gly Lys Lys Tyr Thr Val Gly Thr Ser
          500          505          510
Asp Phe Asn Asn Leu Ala Gln Asn Ile Ala Leu Ala Ala Asp Arg Phe
          515          520          525
Leu Ser Thr Val Gln Leu His Ala His Asn Asn Gly Ser Leu Ala Glu
          530          535          540
Glu Phe Asp Arg Thr Thr Gly Leu Ser Thr Gly Ala Arg Asp Leu Thr
545          550          555          560
Trp Ser His Ala Ser Leu Ile Thr Ala Ser Tyr Ala Lys Ala Gly Ala
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Pro Ala Ala

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<210> 50
<211> 1737
<212> DNA
<213> Rhizopus oryzae

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<212> PRT
<213> Artificial Sequence

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<220>

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<400> 51

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Gln Gly Phe Asn Trp Glu Ser Trp Lys Lys Gln Gly Gly Trp Tyr Asn
 35      40      45
Tyr Leu Leu Gly Arg Val Asp Asp Ile Ala Ala Thr Gly Ala Thr His
 50      55      60
Val Trp Leu Pro Gln Pro Ser His Ser Val Ala Pro Gln Gly Tyr Met
 65      70      75      80
Pro Gly Arg Leu Tyr Asp Leu Asp Ala Ser Lys Tyr Gly Thr His Ala
 85      90      95
Glu Leu Lys Ser Leu Thr Ala Ala Phe His Ala Lys Gly Val Gln Cys
 100     105     110
Val Ala Asp Val Val Ile Asn His Arg Cys Ala Asp Tyr Lys Asp Gly
 115     120     125
Arg Gly Ile Tyr Cys Val Phe Glu Gly Gly Thr Pro Asp Ser Arg Leu
 130     135     140
Asp Trp Gly Pro Asp Met Ile Cys Ser Asp Asp Thr Gln Tyr Ser Asn
 145     150     155     160
Gly Arg Gly His Arg Asp Thr Gly Ala Asp Phe Ala Ala Ala Pro Asp
 165     170     175
Ile Asp His Leu Asn Pro Arg Val Gln Gln Glu Leu Ser Asp Trp Leu
 180     185     190
Asn Trp Leu Lys Ser Asp Leu Gly Phe Asp Gly Trp Arg Leu Asp Phe
 195     200     205
Ala Lys Gly Tyr Ser Ala Ala Val Ala Lys Val Tyr Val Asp Ser Thr
 210     215     220
Ala Pro Thr Phe Val Val Ala Glu Ile Trp Ser Ser Leu His Tyr Asp
 225     230     235     240
Gly Asn Gly Glu Pro Ser Ser Asn Gln Asp Ala Asp Arg Gln Glu Leu
 245     250     255
Val Asn Trp Ala Gln Ala Val Gly Gly Pro Ala Ala Ala Phe Asp Phe
 260     265     270
Thr Thr Lys Gly Val Leu Gln Ala Ala Val Gln Gly Glu Leu Trp Arg
 275     280     285
Met Lys Asp Gly Asn Gly Lys Ala Pro Gly Met Ile Gly Trp Leu Pro
 290     295     300
Glu Lys Ala Val Thr Phe Val Asp Asn His Asp Thr Gly Ser Thr Gln
 305     310     315     320
Asn Ser Trp Pro Phe Pro Ser Asp Lys Val Met Gln Gly Tyr Ala Tyr
 325     330     335
Ile Leu Thr His Pro Gly Thr Pro Cys Ile Phe Tyr Asp His Val Phe
 340     345     350
Asp Trp Asn Leu Lys Gln Glu Ile Ser Ala Leu Ser Ala Val Arg Ser
 355     360     365
Arg Asn Gly Ile His Pro Gly Ser Glu Leu Asn Ile Leu Ala Ala Asp
 370     375     380
Gly Asp Leu Tyr Val Ala Lys Ile Asp Asp Lys Val Ile Val Lys Ile
 385     390     395     400
Gly Ser Arg Tyr Asp Val Gly Asn Leu Ile Pro Ser Asp Phe His Ala
 405     410     415
Val Ala His Gly Asn Asn Tyr Cys Val Trp Glu Lys His Gly Leu Arg
 420     425     430

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Val Pro Ala Gly Arg His His
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<210> 52
<211> 1320
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

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aactcgtggc cattccccctc cgacaaggtc atgcagggct acgcctatat cctcacgcac 1020
ccaggaactc catgcatctt ctacgaccac gttttcgact ggaacctgaa gcaggagatc 1080
agcgcgtgtg ctgcggtgag gtcaagaaac gggatccacc cggggagcga gctgaacatc 1140
ctcgccggcg acggggatct ctacgtcgcc aagattgacg acaaggatcat cgtgaagatc 1200
gggtcacggg acgacgtcgg gaacctgatc ccctcagact tccacgccgt tgcccctggc 1260
aacaactact gcgtttggga gaagcacggt ctgagagttc cagcggggcg gcaccactag 1320
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<210> 53
<211> 45
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

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<400> 53
Ala Thr Gly Gly Thr Thr Thr Ala Thr Thr Thr Gly Ser Gly Gly
 1           5           10           15
Val Thr Ser Thr Ser Lys Thr Thr Thr Thr Ala Ser Lys Thr Ser Thr
      20           25           30
Thr Thr Ser Ser Thr Ser Cys Thr Thr Pro Thr Ala Val
      35           40           45
```

<210> 54
<211> 137
<212> DNA
<213> Artificial Sequence

<220>

<223> synthetic

<400> 54

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gccaccggcg gcaccaccac caccgccacc accaccgggt cggcgggcgt gacctccacc 60
tccaagacca ccaccaccgc ctccaagacc tccaccacca cctcctccac ctctgcacc 120
accccgaccg ccgtgtgc                                     137

```

<210> 55

<211> 300

<212> PRT

<213> *Pyrococcus furiosus*

<400> 55

```

Ile Tyr Phe Val Glu Lys Tyr His Thr Ser Glu Asp Lys Ser Thr Ser
1      5      10      15
Asn Thr Ser Ser Thr Pro Pro Gln Thr Thr Leu Ser Thr Thr Lys Val
20      25      30
Leu Lys Ile Arg Tyr Pro Asp Asp Gly Glu Trp Pro Gly Ala Pro Ile
35      40      45
Asp Lys Asp Gly Asp Gly Asn Pro Glu Phe Tyr Ile Glu Ile Asn Leu
50      55      60
Trp Asn Ile Leu Asn Ala Thr Gly Phe Ala Glu Met Thr Tyr Asn Leu
65      70      75      80
Thr Ser Gly Val Leu His Tyr Val Gln Gln Leu Asp Asn Ile Val Leu
85      90      95
Arg Asp Arg Ser Asn Trp Val His Gly Tyr Pro Glu Ile Phe Tyr Gly
100     105     110
Asn Lys Pro Trp Asn Ala Asn Tyr Ala Thr Asp Gly Pro Ile Pro Leu
115     120     125
Pro Ser Lys Val Ser Asn Leu Thr Asp Phe Tyr Leu Thr Ile Ser Tyr
130     135     140
Lys Leu Glu Pro Lys Asn Gly Leu Pro Ile Asn Phe Ala Ile Glu Ser
145     150     155     160
Trp Leu Thr Arg Glu Ala Trp Arg Thr Thr Gly Ile Asn Ser Asp Glu
165     170     175
Gln Glu Val Met Ile Trp Ile Tyr Tyr Asp Gly Leu Gln Pro Ala Gly
180     185     190
Ser Lys Val Lys Glu Ile Val Val Pro Ile Ile Val Asn Gly Thr Pro
195     200     205
Val Asn Ala Thr Phe Glu Val Trp Lys Ala Asn Ile Gly Trp Glu Tyr
210     215     220
Val Ala Phe Arg Ile Lys Thr Pro Ile Lys Glu Gly Thr Val Thr Ile
225     230     235     240
Pro Tyr Gly Ala Phe Ile Ser Val Ala Ala Asn Ile Ser Ser Leu Pro
245     250     255
Asn Tyr Thr Glu Leu Tyr Leu Glu Asp Val Glu Ile Gly Thr Glu Phe
260     265     270
Gly Thr Pro Ser Thr Thr Ser Ala His Leu Glu Trp Trp Ile Thr Asn
275     280     285
Ile Thr Leu Thr Pro Leu Asp Arg Pro Leu Ile Ser
290     295     300

```

<210> 56

<211> 903

<212> DNA

<213> *Pyrococcus furiosus*

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<400> 56
atctacttcg tggagaagta ccacacctcc gaggacaagt ccacctccaa cacctcctcc 60
accccgccgc agaccaccct ctccaccacc aagggtgctca agatccgcta cccggacgac 120
ggcgagtggc cggcgccccc gatcgacaag gacggcgacg gcaaccggga gttctacatc 180
gagatcaacc tctggaacat cctcaacgcc accggcttcg ccgagatgac ctacaacctc 240
actagtggcg tgctccacta cgtgcagcag ctcgacaaca tcgtgctccg cgaccgctcc 300
aactgggtgc acggctaccc ggaaatcttc tacggcaaca agccgtggaa cgccaactac 360
gccaccgacg gcccgatccc gctcccgctc aagggtgtcca acctcaccga cttctacctc 420
accatctcct acaagctcga gccgaagaac ggtctcccga tcaacttcgc catcgagtcc 480
tggctcaccg gcgaggcctg gcgcaccacc ggcatacaact ccgacgagca ggaggtgatg 540
atctggatct actacgacgg cctccagccc gcgggctcca aggtgaagga gatcggtgtg 600
ccgatcatcg tgaacggcac cccggtgaac gccaccttcg aggtgtggaa ggccaacatc 660
ggctgggagt acgtggcctt ccgcatcaag accccgatca aggagggcac cgtgaccatc 720
ccgtacggcg ccttcatctc cgtggccgcc aacatctcct ccctcccgaa ctacaccgag 780
aagtacctcg aggacgtgga gatcggcacc gagttcggca ccccgctcac cacctccgcc 840
cacctcgagt ggtggatcac caacatcacc ctcaccccgc tcgaccgccc gctcatctcc 900
tag 903

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<210> 57

<211> 387

<212> PRT

<213> *Thermus flavus*

<400> 57

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Met Tyr Glu Pro Lys Pro Glu His Arg Phe Thr Phe Gly Leu Trp Thr
1      5      10      15
Val Asp Asn Val Asp Arg Asp Pro Phe Gly Asp Thr Val Arg Glu Arg
20      25      30
Leu Asp Pro Val Tyr Val Val His Lys Leu Ala Glu Leu Gly Ala Tyr
35      40      45
Gly Val Asn Leu His Asp Glu Asp Leu Ile Pro Arg Gly Thr Pro Pro
50      55      60
Gln Glu Arg Asp Gln Ile Val Arg Arg Phe Lys Lys Ala Leu Asp Glu
65      70      75      80
Thr Val Leu Lys Val Pro Met Val Thr Ala Asn Leu Phe Ser Glu Pro
85      90      95
Ala Phe Arg Asp Gly Ala Ser Thr Thr Arg Asp Pro Trp Val Trp Ala
100     105     110
Tyr Ala Leu Arg Lys Ser Leu Glu Thr Met Asp Leu Gly Ala Glu Leu
115     120     125
Gly Ala Glu Ile Tyr Met Phe Trp Met Val Arg Glu Arg Ser Glu Val
130     135     140
Glu Ser Thr Asp Lys Thr Arg Lys Val Trp Asp Trp Val Arg Glu Thr
145     150     155     160
Leu Asn Phe Met Thr Ala Tyr Thr Glu Asp Gln Gly Tyr Gly Tyr Arg
165     170     175
Phe Ser Val Glu Pro Lys Pro Asn Glu Pro Arg Gly Asp Ile Tyr Phe
180     185     190
Thr Thr Val Gly Ser Met Leu Ala Leu Ile His Thr Leu Asp Arg Pro
195     200     205
Glu Arg Phe Gly Leu Asn Pro Glu Phe Ala His Glu Thr Met Ala Gly
210     215     220
Leu Asn Phe Asp His Ala Val Ala Gln Ala Val Asp Ala Gly Lys Leu
225     230     235     240
Phe His Ile Asp Leu Asn Asp Gln Arg Met Ser Arg Phe Asp Gln Asp
245     250     255
Leu Arg Phe Gly Ser Glu Asn Leu Lys Ala Gly Phe Phe Leu Val Asp
260     265     270

```

Leu Leu Glu Ser Ser Gly Tyr Gln Gly Pro Arg His Phe Glu Ala His
 275 280 285
 Ala Leu Arg Thr Glu Asp Glu Glu Gly Val Trp Thr Phe Val Arg Val
 290 295 300
 Cys Met Arg Thr Tyr Leu Ile Ile Lys Val Arg Ala Glu Thr Phe Arg
 305 310 315 320
 Glu Asp Pro Glu Val Lys Glu Leu Leu Ala Tyr Tyr Gln Glu Asp
 325 330 335
 Pro Ala Thr Leu Ala Leu Leu Asp Pro Tyr Ser Arg Glu Lys Ala Glu
 340 345 350
 Ala Leu Lys Arg Ala Glu Leu Pro Leu Glu Thr Lys Arg Arg Arg Gly
 355 360 365
 Tyr Ala Leu Glu Arg Leu Asp Gln Leu Ala Val Glu Tyr Leu Leu Gly
 370 375 380
 Val Arg Gly
 385

<210> 58
 <211> 978
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 58
 atggggaaga acggcaacct gtgctgcttc tctctgctgc tgctttcttct cgccggggttg 60
 gcgtccggcc atcaaatcta cttcgtggag aagtaccaca cctccgagga caagtccacc 120
 tccaacacct cctccacccc gccgcagacc accctctcca ccaccaaggt gctcaagatc 180
 cgctaccggc acgacgggtga gtggcccgcc gccccgatcg acaaggacgg cgacgggcaac 240
 ccggagttct acatcgagat caacctctgg aacatcctca acgccaccgg cttcgccgag 300
 atgacctaca acctcactag tggcgtgctc cactacgtgc agcagctcga caacatcgtg 360
 ctccgcgacc gctccaactg ggtgcacggc taccggaaa tcttctacgg caacaagccg 420
 tggaacgcca actacgccac cgacggcccc atcccgctcc cgtccaaggt gtccaacctc 480
 accgacttct acctcaccat ctctacaag ctcgagccga agaacggtct cccgatcaac 540
 ttcgccatcg agtcctggct caccgcgag gccctggcgca ccaccggcat caactccgac 600
 gagcaggagg tgatgatctg gatctactac gacggcctcc agcccgcggg ctccaagggtg 660
 aaggagatcg tgggtccgat catcgtgaac ggcaccccg tgaacgccac cttcgagggtg 720
 tggaaggcca acatcggtcg ggagtacgtg gccttcogca tcaagacccc gatcaaggag 780
 ggcaccgtga ccatcccgta cggcgccctt atctccgtgg ccgccaacat ctctctccctc 840
 ccgaactaca ccgagaagta cctcgaggac gtggagatcg gcaccgagtt cggcaccgcc 900
 tccaccacct ccgcccacct cgagtgggtg atcaccaaca tcaccctcac cccgctcgac 960
 cgcccgctca tctcctag

<210> 59
 <211> 1920
 <212> DNA
 <213> *Aspergillus niger*

<400> 59
 atgtccttcc gctccctcct cgccctctcc ggctcgtgt gcaccggcct cgccaacgtg 60
 atctccaagc gcgccacct cgactcctgg ctctccaacg aggccaccgt ggcccgacc 120
 gccatcctca acaacatcgg ccgcgacggc gcctgggtgt ccggcgccga ctccggcatc 180
 gtgggtggcct ccccgctccac cgacaacccg gactacttct acacctggac ccgcgactcc 240
 ggctcgtgc tcaagacct cgtggacct ttcgcgaacg gcgacacct cctcctctcc 300
 accatcgaga actacatctc cgcccaggcc atcgtgcagg gcatctccaa cccgtccggc 360
 gacctctcct ccggcgccgg cctcggcgag ccgaagtcca acgtggacga gaccgcctac 420

```

accggctcct  ggggcccggcc  gcagcgcgac  ggcccggccc  tccgcgccac  ~cgccatgac  480
ggcttcggcc  agtggctcct  cgacaacggc  tacacctcca  ccgccaccga  catcgtgtgg  540
ccgctcgtgc  gcaacgacct  ctctacgtg  gccagtgact  ggaaccagac  cggctacgac  600
ctctgggagg  aggtgaacgg  ctctccttc  ttcaccatcg  ccgtgcagca  ccgcgccttc  660
gtggagggct  ccgccttcgc  caccgcccgt  ggctcctcct  gctcctgggt  cgactcccag  720
gccccggaga  tcctctgcta  cctccagtc  ttctggaccg  gctccttcac  cctcgccaac  780
ttcgactcct  cccgctccgg  caaggacgcc  aacaccctcc  tcggctccat  ccacaccttc  840
gaccgcggag  ccgcctgcga  cgactccacc  ttccagccgt  gctccccgcy  cgccctcgcc  900
aaccacaagg  aggtgggtga  ctcttcggc  tccatctaca  ccctcaacga  cggcctctcc  960
gactccgagg  ccgtggccgt  gggccgctac  ccggaggaca  cctactacaa  cggcaaccgc  1020
tggttcctct  gcacctcgc  cgccgcccag  cagctctacg  acgccctcta  ccagtgggac  1080
aagcagggct  ccctcgagg  gaccgacgtg  tccctcgact  tcttcaaggc  cctctactcc  1140
gacgcgcgca  ccggcaccta  ctctcctcc  tctccacct  actcctccat  cgtggacgcc  1200
gtgaagacct  tcgcccagcg  ctctcgttcc  atcgtggaga  cccacgccgc  ctccaacggc  1260
tccatgtccg  agcagtagca  caagtccgac  ggcgagcagc  tctccgccc  cgacctcacc  1320
tggctcctac  ccgcctcct  caccgccaac  aaccgcccga  actccgtgg  gccggcctcc  1380
tggggcgaga  cctccgcctc  ctccgtgccc  ggcacctgcy  ccgccacctc  cgccatcgcc  1440
acctactcct  ccgtgaccgt  gacctcctgg  ccgtccatcg  tggccaccgg  cggcaccacc  1500
accaccgcca  ccccgaccgg  ctccggctcc  gtgacctcca  cctccaagac  caccgccacc  1560
gcctccaaga  cctccacctc  cactcctcc  acctcctgca  ccaccccgac  cgccgtggcc  1620
gtgaccttcg  acctcaccgc  caccaccacc  tacggcgaga  acatctacct  cgtgggctcc  1680
atctcccagc  tcggcgactg  ggagacctcc  gacggcatcg  ccctctccgc  cgacaagtac  1740
acctcctccg  acccgctctg  gtacgtgacc  gtgacctcc  cggccggcgga  gtccttcgag  1800
tacaagttca  tccgcatcga  gtccgacgac  tccgtggagt  gggagtccga  cccgaaccgc  1860
gagtacaccg  tgccgcaggc  ctgcggcacc  tccaccgcca  ccgtgaccga  cacctggcgc  1920

```

<210> 60
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 60
 Ser Glu Lys Asp Glu Leu
 1 5

<210> 61
 <211> 561
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Xylanase BD7436

<220>
 <221> CDS
 <222> (1)..(561)

<400> 61
 atg gct agc acc ttc tac tgg cat ttg tgg acc gac ggc atc ggc acc 48
 Met Ala Ser Thr Phe Tyr Trp His Leu Trp Thr Asp Gly Ile Gly Thr
 1 5 10 15

gtg aac gct acc aac ggc agc gac ggc aac tac agc gtg agc tgg agc	96
Val Asn Ala Thr Asn Gly Ser Asp Gly Asn Tyr Ser Val Ser Trp Ser	
20 25 30	
aac tgc ggc aac ttc gtg gtg ggc aag ggc tgg acc acc ggc agc gct	144
Asn Cys Gly Asn Phe Val Val Gly Lys Gly Trp Thr Thr Gly Ser Ala	
35 40 45	
acc agg gtg atc aac tac aac gct cat gct ttc agc gtg gtg ggc aac	192
Thr Arg Val Ile Asn Tyr Asn Ala His Ala Phe Ser Val Val Gly Asn	
50 55 60	
gct tac ttg gct ttg tac ggc tgg acc agg aac agc ttg atc gag tac	240
Ala Tyr Leu Ala Leu Tyr Gly Trp Thr Arg Asn Ser Leu Ile Glu Tyr	
65 70 75 80	
tac gtg gtg gac agc tgg ggc acc tac agg cca acc ggc acc tac aag	288
Tyr Val Val Asp Ser Trp Gly Thr Tyr Arg Pro Thr Gly Thr Tyr Lys	
85 90 95	
ggc acc gtg acc agc gac ggc ggc acc tac gac atc tac acc acc acc	336
Gly Thr Val Thr Ser Asp Gly Gly Thr Tyr Asp Ile Tyr Thr Thr Thr	
100 105 110	
agg acc aac gct cca agc atc gac ggc aac aac acc acc ttc acc caa	384
Arg Thr Asn Ala Pro Ser Ile Asp Gly Asn Asn Thr Thr Phe Thr Gln	
115 120 125	
ttc tgg agc gtg agg caa agc aag agg cca atc ggc acc aac aac acc	432
Phe Trp Ser Val Arg Gln Ser Lys Arg Pro Ile Gly Thr Asn Asn Thr	
130 135 140	
atc acc ttc agc aac cat gtg aac gct tgg aag agc aag ggc atg aac	480
Ile Thr Phe Ser Asn His Val Asn Ala Trp Lys Ser Lys Gly Met Asn	
145 150 155 160	
ttg ggc agc agc tgg agc tac caa gtg ttg gct acc gag ggc tac caa	528
Leu Gly Ser Ser Trp Ser Tyr Gln Val Leu Ala Thr Glu Gly Tyr Gln	
165 170 175	
agc agc ggc tac agc aac gtg acc gtg tgg tag	561
Ser Ser Gly Tyr Ser Asn Val Thr Val Trp	
180 185	

<210> 62
 <211> 186
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Synthetic Construct

 <400> 62

Met Ala Ser Thr Phe Tyr Trp His Leu Trp Thr Asp Gly Ile Gly Thr
1 5 10 15

Val Asn Ala Thr Asn Gly Ser Asp Gly Asn Tyr Ser Val Ser Trp Ser
 20 25 30
 Asn Cys Gly Asn Phe Val Val Gly Lys Gly Trp Thr Thr Gly Ser Ala
 35 40 45
 Thr Arg Val Ile Asn Tyr Asn Ala His Ala Phe Ser Val Val Gly Asn
 50 55 60
 Ala Tyr Leu Ala Leu Tyr Gly Trp Thr Arg Asn Ser Leu Ile Glu Tyr
 65 70 75 80
 Tyr Val Val Asp Ser Trp Gly Thr Tyr Arg Pro Thr Gly Thr Tyr Lys
 85 90 95
 Gly Thr Val Thr Ser Asp Gly Gly Thr Tyr Asp Ile Tyr Thr Thr Thr
 100 105 110
 Arg Thr Asn Ala Pro Ser Ile Asp Gly Asn Asn Thr Thr Phe Thr Gln
 115 120 125
 Phe Trp Ser Val Arg Gln Ser Lys Arg Pro Ile Gly Thr Asn Asn Thr
 130 135 140
 Ile Thr Phe Ser Asn His Val Asn Ala Trp Lys Ser Lys Gly Met Asn
 145 150 155 160
 Leu Gly Ser Ser Trp Ser Tyr Gln Val Leu Ala Thr Glu Gly Tyr Gln
 165 170 175
 Ser Ser Gly Tyr Ser Asn Val Thr Val Trp
 180 185

<210> 63
 <211> 561
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Xylanase BD6002A

<220>
 <221> CDS
 <222> (1)..(561)

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<400> 63
atg gct agc acc gac tac tgg caa aac tgg acc gac ggc ggc ggc acc 48
Met Ala Ser Thr Asp Tyr Trp Gln Asn Trp Thr Asp Gly Gly Gly Thr
1 5 10 15

gtg aac gct acc aac ggc agc gac ggc aac tac agc gtg agc tgg agc 96
Val Asn Ala Thr Asn Gly Ser Asp Gly Asn Tyr Ser Val Ser Trp Ser
20 25 30

aac tgc ggc aac ttc gtg gtg ggc aag ggc tgg acc acc ggc agc gct 144
Asn Cys Gly Asn Phe Val Val Gly Lys Gly Trp Thr Thr Gly Ser Ala
35 40 45

acc agg gtg atc aac tac aac gct ggc gct ttc agc cca agc ggc aac 192
Thr Arg Val Ile Asn Tyr Asn Ala Gly Ala Phe Ser Pro Ser Gly Asn
50 55 60

ggc tac ttg gct ttg tac ggc tgg acc agg aac agc ttg atc gag tac 240
Gly Tyr Leu Ala Leu Tyr Gly Trp Thr Arg Asn Ser Leu Ile Glu Tyr
65 70 75 80

tac gtg gtg gac agc tgg ggc acc tac agg cca acc ggc acc tac aag 288
Tyr Val Val Asp Ser Trp Gly Thr Tyr Arg Pro Thr Gly Thr Tyr Lys
85 90 95

ggc acc gtg acc agc gac ggc ggc acc tac gac atc tac acc acc acc 336
Gly Thr Val Thr Ser Asp Gly Gly Thr Tyr Asp Ile Tyr Thr Thr Thr
100 105 110

agg acc aac gct cca agc atc gac ggc aac aac acc acc ttc acc caa 384
Arg Thr Asn Ala Pro Ser Ile Asp Gly Asn Asn Thr Thr Phe Thr Gln
115 120 125

ttc tgg agc gtg agg caa agc aag agg cca atc ggc acc aac aac acc 432
Phe Trp Ser Val Arg Gln Ser Lys Arg Pro Ile Gly Thr Asn Asn Thr
130 135 140

atc acc ttc agc aac cat gtg aac gct tgg aag agc aag ggc atg aac 480
Ile Thr Phe Ser Asn His Val Asn Ala Trp Lys Ser Lys Gly Met Asn
145 150 155 160

ttg ggc agc agc tgg agc tac caa gtg ttg gct acc gag ggc tac caa 528
Leu Gly Ser Ser Trp Ser Tyr Gln Val Leu Ala Thr Glu Gly Tyr Gln
165 170 175

agc agc ggc tac agc aac gtg acc gtg tgg tag 561
Ser Ser Gly Tyr Ser Asn Val Thr Val Trp
180 185

<210> 64
<211> 186
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

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<400> 64

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Met Ala Ser Thr Asp Tyr Trp Gln Asn Trp Thr Asp Gly Gly Gly Thr
1          5          10          15

Val Asn Ala Thr Asn Gly Ser Asp Gly Asn Tyr Ser Val Ser Trp Ser
          20          25          30

Asn Cys Gly Asn Phe Val Val Gly Lys Gly Trp Thr Thr Gly Ser Ala
          35          40          45

Thr Arg Val Ile Asn Tyr Asn Ala Gly Ala Phe Ser Pro Ser Gly Asn
          50          55          60

Gly Tyr Leu Ala Leu Tyr Gly Trp Thr Arg Asn Ser Leu Ile Glu Tyr
65          70          75          80

Tyr Val Val Asp Ser Trp Gly Thr Tyr Arg Pro Thr Gly Thr Tyr Lys
          85          90          95

Gly Thr Val Thr Ser Asp Gly Gly Thr Tyr Asp Ile Tyr Thr Thr Thr
          100          105          110

Arg Thr Asn Ala Pro Ser Ile Asp Gly Asn Asn Thr Thr Phe Thr Gln
          115          120          125

Phe Trp Ser Val Arg Gln Ser Lys Arg Pro Ile Gly Thr Asn Asn Thr
          130          135          140

Ile Thr Phe Ser Asn His Val Asn Ala Trp Lys Ser Lys Gly Met Asn
145          150          155          160

Leu Gly Ser Ser Trp Ser Tyr Gln Val Leu Ala Thr Glu Gly Tyr Gln
          165          170          175

Ser Ser Gly Tyr Ser Asn Val Thr Val Trp
          180          185

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<210> 65
 <211> 561
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Xylanase BD6002B


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<220>
<221> CDS
<222> (1)..(561)

<400> 65
atg gcc tcc acc gac tac tgg cag aac tgg acc gac ggc ggc ggc acc      48
Met Ala Ser Thr Asp Tyr Trp Gln Asn Trp Thr Asp Gly Gly Gly Thr
1          5          10          15

gtg aac gcc acc aac ggc tcc gac ggc aac tac tcc gtg tcc tgg tcc      96
Val Asn Ala Thr Asn Gly Ser Asp Gly Asn Tyr Ser Val Ser Trp Ser
20          25          30

aac tgc ggc aac ttc gtg gtg ggc aag ggc tgg acc acc ggc tcc gcc      144
Asn Cys Gly Asn Phe Val Val Gly Lys Gly Trp Thr Thr Gly Ser Ala
35          40          45

acc cgc gtg atc aac tac aac gcc ggc gcc ttc tcc ccg tcc ggc aac      192
Thr Arg Val Ile Asn Tyr Asn Ala Gly Ala Phe Ser Pro Ser Gly Asn
50          55          60

ggc tac ctc gcc ctc tac ggc tgg acc cgc aac tcc ctc atc gag tac      240
Gly Tyr Leu Ala Leu Tyr Gly Trp Thr Arg Asn Ser Leu Ile Glu Tyr
65          70          75          80

tac gtg gtg gac tcc tgg ggc acc tac cgc ccg acc ggc acc tac aag      288
Tyr Val Val Asp Ser Trp Gly Thr Tyr Arg Pro Thr Gly Thr Tyr Lys
85          90          95

ggc acc gtg acc tcc gac ggc ggc acc tac gac atc tac acc acc acc      336
Gly Thr Val Thr Ser Asp Gly Gly Thr Tyr Asp Ile Tyr Thr Thr Thr
100         105         110

cgc acc aac gcc ccg tcc atc gac ggc aac aac acc acc ttc acc cag      384
Arg Thr Asn Ala Pro Ser Ile Asp Gly Asn Asn Thr Thr Phe Thr Gln
115         120         125

ttc tgg tcc gtg cgc cag tcc aag cgc ccg atc ggc acc aac aac acc      432
Phe Trp Ser Val Arg Gln Ser Lys Arg Pro Ile Gly Thr Asn Asn Thr
130         135         140

atc acc ttc tcc aac cac gtg aac gcc tgg aag tcc aag ggc atg aac      480
Ile Thr Phe Ser Asn His Val Asn Ala Trp Lys Ser Lys Gly Met Asn
145         150         155         160

ctc ggc tcc tcc tgg tcc tac cag gtg ctc gcc acc gag ggc tac cag      528
Leu Gly Ser Ser Trp Ser Tyr Gln Val Leu Ala Thr Glu Gly Tyr Gln
165         170         175

tcc tcc ggc tac tcc aac gtg acc gtg tgg tga      561
Ser Ser Gly Tyr Ser Asn Val Thr Val Trp
180         185

<210> 66
<211> 186

```

<212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 66

Met Ala Ser Thr Asp Tyr Trp Gln Asn Trp Thr Asp Gly Gly Gly Thr
 1 5 10 15

Val Asn Ala Thr Asn Gly Ser Asp Gly Asn Tyr Ser Val Ser Trp Ser
 20 25 30

Asn Cys Gly Asn Phe Val Val Gly Lys Gly Trp Thr Thr Gly Ser Ala
 35 40 45

Thr Arg Val Ile Asn Tyr Asn Ala Gly Ala Phe Ser Pro Ser Gly Asn
 50 55 60

Gly Tyr Leu Ala Leu Tyr Gly Trp Thr Arg Asn Ser Leu Ile Glu Tyr
 65 70 75 80

Tyr Val Val Asp Ser Trp Gly Thr Tyr Arg Pro Thr Gly Thr Tyr Lys
 85 90 95

Gly Thr Val Thr Ser Asp Gly Gly Thr Tyr Asp Ile Tyr Thr Thr Thr
 100 105 110

Arg Thr Asn Ala Pro Ser Ile Asp Gly Asn Asn Thr Thr Phe Thr Gln
 115 120 125

Phe Trp Ser Val Arg Gln Ser Lys Arg Pro Ile Gly Thr Asn Asn Thr
 130 135 140

Ile Thr Phe Ser Asn His Val Asn Ala Trp Lys Ser Lys Gly Met Asn
 145 150 155 160

Leu Gly Ser Ser Trp Ser Tyr Gln Val Leu Ala Thr Glu Gly Tyr Gln
 165 170 175

Ser Ser Gly Tyr Ser Asn Val Thr Val Trp
 180 185

<210> 67
 <211> 2071

<212> DNA
 <213> *Oryza sativa*

<220>
 <221> misc_feature
 <222> (1)..(2071)
 <223> Promoter

<400> 67
 tccatgctgt cctactactt gcttcatccc cttctacatt ttgttctggt ttttggcctg 60
 catttcggat catgatgtat gtgatttcca atctgctgca atatgaatgg agactctgtg 120
 ctaaccatca acaacatgaa atgcttatga ggcctttgct gagcagccaa tcttgccctg 180
 gtttatgtct tcacaggccg aattcctctg ttttgttttt caccctcaat atttggaac 240
 atttatctag gttgtttgtg tccaggccta taaatcatac atgatgttgt cgtattggat 300
 gtgaatgtgg tggcgtgttc agtgcccttg atttgagttt gatgagagtt gcttctgggt 360
 caccactcac cattatcgat gctcctcttc agcataaggt aaaagtcttc cctgtttacg 420
 ttattttacc cactatgggt gcttggggtg gtttttctct gattgcttat gccatggaaa 480
 gtcatttgat atgttgaact tgaattaact gtagaattgt atacatgttc catttggtgt 540
 gtacttcctt cttttctatt agtagcctca gatgagtggt aaaaaaacag attatataac 600
 ttgccctata aatcatttga aaaaaatatt gtacagttag aaattgatat atagtgaatt 660
 ttttaagagca tgttttccta aagaagtata tattttctat gtacaaaggc cattgaagta 720
 attgtagata caggataatg tagacttttt ggacttacac tgctaccttt aagtaacaat 780
 catgagcaat agtggtgcaa tgatatttag gctgcattcg tttactctct tgatttccat 840
 gagcacgctt cccaaactgt taaactctgt gttttttgcc aaaaaaaaaat gcataggaaa 900
 gttgctttta aaaaatcata tcaatccatt ttttaagtta tagctaatac ttaattaatc 960
 atgcgctaata aagtcactct gtttttcgta ctagagagat tgttttgaac cagcactcaa 1020
 gaacacagcc ttaaccagc caaataatgc tacaacctac cagtccacac ctcttgtaaa 1080
 gcatttggtg catggaaaag ctaagatgac agcaacctgt tcaggaaaac aactgacaag 1140
 gtcataggga gagggagctt ttggaaagggt gccgtgcagt tcaaacaatt agttagcagt 1200
 aggggtgttg tttttgctca cagcaataag aagttaatca tgggtgtaggc aacccaaata 1260
 aaacacaaaa atatgcacaa ggcagtttgt tgtattctgt agtacagaca aaactaaaag 1320
 taatgaaaga agatgtggtg ttagaaaagg aaacaatatc atgagtaatg tgtgggcatt 1380
 atgggaccac gaaataaaaa gaacattttg atgagtcgtg tatcctcgat gagcctcaaa 1440

```

agttctctca ccccgataa gaaaccctta agcaatgtgc aaagtttgca ttctccactg 1500
acataatgca aaataagata tcatcgatga catagcaact catgcatcat atcatgcctc 1560
tctcaaccta ttcattccta ctcatctaca taagtatctt cagctaaatg ttagaacata 1620
aaccataag tcacgtttga tgagtattag gcgtgacaca tgacaaatca cagactcaag 1680
caagataaag caaaatgatg tgtacataaa actccagagc tatatgtcat attgcaaaaa 1740
gaggagagct tataagacaa ggcatgactc aaaaaaattc atttgccctt cgtgtcaaaa 1800
agaggagggc tttacattat ccatgtcata ttgcaaaaaga aagagagaaa gaacaacaca 1860
atgctgcgtc aattatacat atctgtatgt ccatcattat tcatccacct ttcgtgtacc 1920
acacttcata tatcatgagt cacttcatgt ctggacatta aaaaactcta tcttaacatt 1980
tagatgcaag agcctttatc tcaactataaa tgcacgatga tttctcattg tttctcacia 2040
aaagcattca gttcattagt cctacaacaa c 2071

```

```

<210> 68
<211> 79
<212> PRT
<213> Zea mays

```

```

<220>
<221> SIGNAL
<222> (1)..(79)
<223> Maize waxy signal sequence.

```

```

<400> 68

```

```

Met Leu Ala Ala Leu Ala Thr Ser Gln Leu Val Ala Thr Arg Ala Gly
1           5           10           15

```

```

Leu Gly Val Pro Asp Ala Ser Thr Phe Arg Arg Gly Ala Ala Gln Gly
          20           25           30

```

```

Leu Arg Gly Ala Arg Ala Ser Ala Ala Ala Asp Thr Leu Ser Met Arg
          35           40           45

```

```

Thr Ser Ala Arg Ala Ala Pro Arg His Gln His Gln Gln Ala Arg Arg
          50           55           60

```

```

Gly Ala Arg Phe Pro Ser Leu Val Val Cys Ala Ser Ala Gly Ala
65           70           75

```

```

<210> 69
<211> 1005

```

<212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Bromelain Sequence

<220>
 <221> CDS
 <222> (1)..(1005)
 <223> Synthetic Bromelain

```

<400> 69
atg gcc tgg aag gtg cag gtg gtg ttc ctc ttc ctc ttc ctc tgc gtg      48
Met Ala Trp Lys Val Gln Val Val Phe Leu Phe Leu Phe Leu Cys Val
1          5          10          15

atg tgg gcc tcc ccg tcc gcc gcc tcc gcg gac gag ccg tcc gac ccg      96
Met Trp Ala Ser Pro Ser Ala Ala Ser Ala Asp Glu Pro Ser Asp Pro
          20          25          30

atg atg aag cgc ttc gag gag tgg atg gtg gag tac ggc cgc gtg tac      144
Met Met Lys Arg Phe Glu Glu Trp Met Val Glu Tyr Gly Arg Val Tyr
          35          40          45

aag gac aac gac gag aag atg cgc cgc ttc cag atc ttc aag aac aac      192
Lys Asp Asn Asp Glu Lys Met Arg Arg Phe Gln Ile Phe Lys Asn Asn
          50          55          60

gtg aac cac atc gag acc ttc aac tcc cgc aac gag aac tcc tac acc      240
Val Asn His Ile Glu Thr Phe Asn Ser Arg Asn Glu Asn Ser Tyr Thr
          65          70          75          80

ctc ggc atc aac cag ttc acc gac atg acc aac aac gag ttc atc gcc      288
Leu Gly Ile Asn Gln Phe Thr Asp Met Thr Asn Asn Glu Phe Ile Ala
          85          90          95

cag tac acc ggc ggc atc tcc cgc ccg ctc aac atc gag cgc gag ccg      336
Gln Tyr Thr Gly Gly Ile Ser Arg Pro Leu Asn Ile Glu Arg Glu Pro
          100          105          110

gtg gtg tcc ttc gac gac gtg gac atc tcc gcc gtg ccg cag tcc atc      384
Val Val Ser Phe Asp Asp Val Asp Ile Ser Ala Val Pro Gln Ser Ile
          115          120          125

gac tgg cgc gac tac ggc gcc gtg acc tcc gtg aag aac cag aac ccg      432
Asp Trp Arg Asp Tyr Gly Ala Val Thr Ser Val Lys Asn Gln Asn Pro
          130          135          140

tgc ggc gcc tgc tgg gcc ttc gcc gcc atc gcc acc gtg gag tcc atc      480
Cys Gly Ala Cys Trp Ala Phe Ala Ala Ile Ala Thr Val Glu Ser Ile
          145          150          155          160

tac aag atc aag aag ggc atc ctc gag ccg ctc tcc gag cag cag gtg      528
Tyr Lys Ile Lys Lys Gly Ile Leu Glu Pro Leu Ser Glu Gln Gln Val
          165          170          175

ctc gac tgc gcc aag ggc tac ggc tgc aag ggc ggc tgg gag ttc cgc      576

```

Leu Asp Cys Ala Lys Gly Tyr Gly Cys Lys Gly Gly Trp Glu Phe Arg
 180 185 190
 gcc ttc gag ttc atc atc tcc aac aag ggc gtg gcc tcc ggc gcc atc 624
 Ala Phe Glu Phe Ile Ile Ser Asn Lys Gly Val Ala Ser Gly Ala Ile
 195 200 205
 tac ccg tac aag gcc gcc aag ggc acc tgc aag acc gac ggc gtg ccg 672
 Tyr Pro Tyr Lys Ala Ala Lys Gly Thr Cys Lys Thr Asp Gly Val Pro
 210 215 220
 aac tcc gcc tac atc acc ggc tac gcc cgc gtg ccg cgc aac aac gag 720
 Asn Ser Ala Tyr Ile Thr Gly Tyr Ala Arg Val Pro Arg Asn Asn Glu
 225 230 235 240
 tcc tcc atg atg tac gcc gtg tcc aag cag ccg atc acc gtg gcc gtg 768
 Ser Ser Met Met Tyr Ala Val Ser Lys Gln Pro Ile Thr Val Ala Val
 245 250 255
 gac gcc aac gcc aac ttc cag tac tac aag tcc ggc gtg ttc aac ggc 816
 Asp Ala Asn Ala Asn Phe Gln Tyr Tyr Lys Ser Gly Val Phe Asn Gly
 260 265 270
 ccg tgc ggc acc tcc ctc aac cac gcc gtg acc gcc atc ggc tac ggc 864
 Pro Cys Gly Thr Ser Leu Asn His Ala Val Thr Ala Ile Gly Tyr Gly
 275 280 285
 cag gac tcc atc atc tac ccg aag aag tgg ggc gcc aag tgg ggc gag 912
 Gln Asp Ser Ile Ile Tyr Pro Lys Lys Trp Gly Ala Lys Trp Gly Glu
 290 295 300
 gcc ggc tac atc cgc atg gcc cgc gac gtg tcc tcc tcc tcc ggc atc 960
 Ala Gly Tyr Ile Arg Met Ala Arg Asp Val Ser Ser Ser Ser Gly Ile
 305 310 315 320
 tgc ggc atc gcc atc gac ccg ctc tac ccg acc ctc gag gag tag 1005
 Cys Gly Ile Ala Ile Asp Pro Leu Tyr Pro Thr Leu Glu Glu
 325 330

<210> 70
 <211> 334
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 70

Met Ala Trp Lys Val Gln Val Val Phe Leu Phe Leu Phe Leu Cys Val
 1 5 10 15

Met Trp Ala Ser Pro Ser Ala Ala Ser Ala Asp Glu Pro Ser Asp Pro
 20 25 30

Met Met Lys Arg Phe Glu Glu Trp Met Val Glu Tyr Gly Arg Val Tyr
 35 40 45
 Lys Asp Asn Asp Glu Lys Met Arg Arg Phe Gln Ile Phe Lys Asn Asn
 50 55 60
 Val Asn His Ile Glu Thr Phe Asn Ser Arg Asn Glu Asn Ser Tyr Thr
 65 70 75 80
 Leu Gly Ile Asn Gln Phe Thr Asp Met Thr Asn Asn Glu Phe Ile Ala
 85 90 95
 Gln Tyr Thr Gly Gly Ile Ser Arg Pro Leu Asn Ile Glu Arg Glu Pro
 100 105 110
 Val Val Ser Phe Asp Asp Val Asp Ile Ser Ala Val Pro Gln Ser Ile
 115 120 125
 Asp Trp Arg Asp Tyr Gly Ala Val Thr Ser Val Lys Asn Gln Asn Pro
 130 135 140
 Cys Gly Ala Cys Trp Ala Phe Ala Ala Ile Ala Thr Val Glu Ser Ile
 145 150 155 160
 Tyr Lys Ile Lys Lys Gly Ile Leu Glu Pro Leu Ser Glu Gln Gln Val
 165 170 175
 Leu Asp Cys Ala Lys Gly Tyr Gly Cys Lys Gly Gly Trp Glu Phe Arg
 180 185 190
 Ala Phe Glu Phe Ile Ile Ser Asn Lys Gly Val Ala Ser Gly Ala Ile
 195 200 205
 Tyr Pro Tyr Lys Ala Ala Lys Gly Thr Cys Lys Thr Asp Gly Val Pro
 210 215 220
 Asn Ser Ala Tyr Ile Thr Gly Tyr Ala Arg Val Pro Arg Asn Asn Glu
 225 230 235 240
 Ser Ser Met Met Tyr Ala Val Ser Lys Gln Pro Ile Thr Val Ala Val
 245 250 255
 Asp Ala Asn Ala Asn Phe Gln Tyr Tyr Lys Ser Gly Val Phe Asn Gly
 260 265 270

Pro Cys Gly Thr Ser Leu Asn His Ala Val Thr Ala Ile Gly Tyr Gly
 275 280 285

Gln Asp Ser Ile Ile Tyr Pro Lys Lys Trp Gly Ala Lys Trp Gly Glu
 290 295 300

Ala Gly Tyr Ile Arg Met Ala Arg Asp Val Ser Ser Ser Ser Gly Ile
 305 310 315 320

Cys Gly Ile Ala Ile Asp Pro Leu Tyr Pro Thr Leu Glu Glu
 325 330

<210> 71
 <211> 78
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Bromealin signal sequence

<400> 71
 atggcctgga aggtgcaggt ggtgttcttc ttcctcttcc tctgcgtgat gtgggcctcc 60
 ccgtccgcgc cctccgcc 78

<210> 72
 <211> 26
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Bromealin signal peptide

<400> 72
 Met Ala Trp Lys Val Gln Val Val Phe Leu Phe Leu Phe Leu Cys Val
 1 5 10 15

Met Trp Ala Ser Pro Ser Ala Ala Ser Ala
 20 25

<210> 73
 <211> 1050
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> pSYN11000


```

<400> 73
atggcctgga aggtgcaggt ggtgttcctc ttctcttctc tctgcgtgat gtgggcctcc 60
ccgtccgccg cctccgcgga cgagccgtcc gacccgatga tgaagcgctt cgaggagtgg 120
atggtggagt acggccgcgt gtacaaggac aacgacgaga agatgcgccg cttccagatc 180
ttcaagaaca acgtgaacca catcgagacc ttcaactccc gcaacgagaa ctctacacc 240
ctcggcatca accagttcac cgacatgacc aacaacgagt tcatcgccca gtacaccggc 300
ggcatctccc gcccgctcaa catcgagcgc gagccggtgg tgtccttoga cgacgtggac 360
atctccgccg tgccgcagtc catcgactgg cgcgactacg gcgccgtgac ctccgtgaag 420
aaccagaacc cgtgcggcgc ctgctgggcc ttgcgcgcca tcgccaccgt ggagtccatc 480
tacaagatca agaaggcat cctcgagccg ctctccgagc agcaggtgct cgactgcgcc 540
aagggctacg gctgcaaggg cggctgggag ttccgcgcct tcgagttcat catctccaac 600
aagggcgtgg cctccggcgc catctaccgc tacaaggccg ccaagggcac ctgcaagacc 660
gacggcgtgc cgaactccgc ctacatcacc ggctacgcc gcgtgccgcg caacaacgag 720
tcctccatga tgtacgccgt gtccaagcag ccgatcaccg tggccgtgga cgccaacgcc 780
aacttcagat actacaagtc cggcgtgttc aacggcccgt gcggcaacct cctcaaccac 840
gccgtgaccg ccatcggtta cggccaggac tccatcatct acccgaagaa gtggggcgcc 900
aagtggggcg aggcgggcta catccgcatg gcccgcgacg tgtcctctc ctccggcatc 960
tgccgcatcg ccatcgaccc gctctaccgc accctcgagg aggtgttcgc cgaggccatc 1020
gccgccaact ccaccctcgt ggccgagtag . 1050

```

```

<210> 74
<211> 1067
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> pSYN11589

```

```

<400> 74
tggcctggaa ggtgcaggtg gtgttctctt ttctcttctc ctgcgtgatg tgggcctccc 60
cgtccgccgc ctccgcctcc ttctctctct tcgccgactc caacccgatc cgcccggtga 120
ccgaccgcgc cgctccacc gacgagccgt ccgaccgat gatgaagcgc ttcgaggagt 180
ggatggtgga gtacggccgc gtgtacaagg acaacgacga gaagatgcgc cgcttcaga 240
tcttcaagaa caacgtgaac cacatcgaga ccttcaactc ccgcaacgag aactcctaca 300
cctcggcat caaccagttc accgacatga ccaacaacga gttcatcgcc cagtacaccg 360

```

```

gcggcacatc cgcgccgctc aacatcgagc gcgagccggt ggtgtccttc gacgacgtgg 420
acatctccgc cgtgccgcag tccatcgact ggcgcgacta cggcgccgtg acctccgtga 480
agaaccagaa cccgtgcggc gcctgctggg ccttcgccgc catcgccacc gtggagtcca 540
tctacaagat caagaagggc atcctcgagc cgctctccga gcagcaggtg ctcgactgcg 600
ccaagggcta cggctgcaag ggctgctggg agttccgcgc cttcgagttc atcatctcca 660
acaagggcgt ggctccggc gccatctacc cgtacaaggc cgccaagggc acctgcaaga 720
ccgacggcgt gccgaactcc gcctacatca ccggtacgc ccgctgccg cgcaacaacg 780
agtccctccat gatgtacgcc gtgtccaagc agccgatcac cgtggccgtg gacgccaacg 840
ccaacttcca gtactacaag tccggcgtgt tcaacggccc gtgcggcacc tccctcaacc 900
acgccgtgac cgccatcggc tacggccagg actccatcat ctaccgaag aagtggggcg 960
ccaagtgggg cgaggccggc tacatccgca tggcccgcga cgtgtcctcc tccctcggca 1020
tctgcggcat cgccatcgac ccgctctacc cgaccctcga ggagtag 1067

```

```

<210> 75
<211> 1023
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> pSYN11587 Sequence

```

```

<400> 75
atggcctgga aggtgcaggt ggtgttcctc ttccctcttc tctgcgtgat gtgggcctcc 60
ccgtccgccg cctccgcgga cgagccgtcc gaccgatga tgaagcgctt cgaggagtgg 120
atggtggagt acggccgcgt gtacaaggac aacgacgaga agatgcgccg cttccagatc 180
ttcaagaaca acgtgaacca catcgagacc ttcaactccc gcaacgagaa ctctacacc 240
ctcggcatca accagttcac cgacatgacc aacaacgagt tcatcgccca gtacaccggc 300
ggcatctccc gcccgctcaa catcgagcgc gagccggtgg tgtccttcga cgacgtggac 360
atctccgccg tgccgcagtc catcgactgg cgcgactacg gcgccgtgac ctccgtgaag 420
aaccagaacc cgtgcggcgc ctgctgggccc ttgcgcgcca tcgccaccgt ggagtccatc 480
tacaagatca agaagggcat cctcgagccg ctctccgagc agcaggtgct cgactgcgcc 540
aagggctacg gctgcaaggg cggctgggag ttccgcgcct tcgagttcat catctccaac 600
aagggcgtgg cctccggcgc catctacccg tacaaggccg ccaagggcac ctgcaagacc 660
gacggcgtgc cgaactccgc ctacatcacc ggctacgccc gcgtgccgcg caacaacgag 720

```

```

tccctccatga tgtacgccgt gtccaagcag ccgatcaccg tggccgtgga cgccaacgcc      780
aacttccagt actacaagtc cggcgtgttc aacggcccgt gcggcacctc cctcaaccac      840
gccgtgaccg ccatcggcta cggccaggac tccatcatct acccgaagaa gtggggcgcc      900
aagtggggcg aggcgggcta catccgcatt gcccgcgacg tgtcctctc ctccggcatc      960
tgccggcatcg ccatcgaccc gctctaccgg accctcgagg agtccgagaa ggacgagctg     1020
tag                                                                    1023

```

```

<210> 76
<211> 990
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> pSYN12169 Sequence

```

```

<400> 76
atgagggtgt tgctcgttgc cctcgctctc ctggctctcg ctgcgagcgc cacctccatg      60
gcggacgagc cgtccgaccc gatgatgaag cgcttcgagg agtggaagggt ggagtacggc     120
cgcgtgtaca aggacaacga cgagaagatg cgcgcgttcc agatcttcaa gaacaacgtg     180
aaccacatcg agaccttcaa ctcccgcaac gagaactcct acaccctcgg catcaaccag     240
ttcaccgaca tgaccaacaa cgagttcatc gcccagtaca ccggcgggcat ctcccgcccg     300
ctcaacatcg agcgcgagcc ggtgggtgtcc ttgcagcagc tggacatctc cgccgtgccg     360
cagtccatcg actggcgaga ctacggcgcc gtgacctcgg tgaagaacca gaaccggtgc     420
ggcgccctgt gggccttcgc cgccatcgcc accgtggagt ccatctacaa gatcaagaag     480
ggcatcctcg agccgctctc cgagcagcag gtgctcgact gcgccaaggg ctacggctgc     540
aagggcggct gggagtcccg cgccttcgag ttcatcatct ccaacaaggg cgtggcctcc     600
ggcgccatct acccgtaaa ggccgccaag ggcacctgca agaccgacgg cgtgccgaac     660
tcgccttaca tcaccggcta cgcccgcggt ccgcgcaaca acgagtcctc catgatgtac     720
gccgtgtcca agcagccgat caccgtggcc gtggacgcca acgccaactt ccagtactac     780
aagtccggcg tgttcaacgg cccgtgcggc acctccctca accacgccgt gaccgccatc     840
ggctacggcc aggactccat catctaccgg aagaagtggg gcgccaagtg gggcgaggcc     900
ggctacatcc gcatggcccg cgacgtgtcc tcctcctcgg gcatctgcgg catcgccatc     960
gacccgctct acccgacctt cgaggagtag                                                                    990

```

<210> 77
 <211> 1170
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> pSYN12575 Sequence

```

<400> 77
atgctggcgg ctctggccac gtcgcagctc gtcgcaacgc gcgccggcct gggcgctccc 60
gacgcgtcca cgttcgcgcg cggcgccgcg cagggcctga ggggggcccg ggcgtcggcg 120
gcggcggaca cgctcagcat gcggaccagc gcgcgcgcgg cggccaggca ccagcaccag 180
caggcgcgcc gcggggccag gttcccgtcg ctcgctcgtgt gcgccagcgc cggcgccatg 240
gcggacgagc cgtccgaccc gatgatgaag cgcttcgagg agtggatggt ggagtacggc 300
cgcggtgtaca aggacaacga cgagaagatg cgcgcgttcc agatcttcaa gaacaacgtg 360
aaccacatcg agaccttcaa ctcccgcac gagaaactcct acaccctcgg catcaaccag 420
ttcaccgaca tgaccaacaa cgagttcatc gcccagtaca ccggcggcat ctcccggccc 480
ctcaacatcg agcgcgagcc ggtgggtgtc ttcgacgacg tggacatctc cgccgtgccc 540
cagtcctatc actggcgcgga ctacggcgcc gtgacctccg tgaagaacca gaaccggtgc 600
ggcgccctgct gggccttcgc cgccatcgcc accgtggagt ccatctacaa gatcaagaag 660
ggcatcctcg agcgcgtctc cgagcagcag gtgctcgact gcgccaaggg ctacggctgc 720
aagggcggct gggagttccg cgccttcgag ttcatcatct ccaacaaggg cgtggcctcc 780
ggcgccatct acccgtagaa ggccgccaag ggcacctgca agaccgacgg cgtgccgaac 840
tcgccttaca tcaccggcta cgcccgcggt cgcgcaacaa acgagtcctc catgatgtac 900
gccgtgtcca agcagccgat caccgtggcc gtggacgcca acgccaactt ccagtactac 960
aagtccggcg tgttcaacgg ccgctgcggc acctccctca accacgccgt gaccgccatc 1020
ggctacggcc aggactccat catctacccg aagaagtggg gcgccaagtg gggcgaggcc 1080
ggctacatcc gcatggcccg cgacgtgtcc tcctcctccg gcatctgcgg catcgccatc 1140
gaaccgctct acccgaccct cgaggagtag 1170

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<210> 78
 <211> 1068
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> pSM270 Sequence

```

<400> 78
atggcctgga aggtgcaggt ggtgttctc ttcctcttcc tctgcgtgat gtgggcctcc      60
ccgtccgcgc cctccgcctc ctctctctcc ttgcgcgact ccaacccgat ccgcccggtg      120
accgaccgcg ccgcctccac cgacgagccg tccgaccoga tgatgaagcg cttcgaggag      180
tggatggtgg agtacggccg cgtgtacaag gacaacgacg agaagatgcg ccgcttccag      240
atcttcaaga acaacgtgaa ccacatcgag accttcaact cccgcaacga gaactcctac      300
accctcggca tcaaccagtt caccgacatg accaacaacg agttcatcgc ccagtacacc      360
ggcggcatct cccgcccgcg caacatcgag cgcgagccgg tgggtgtcctt cgacgacgtg      420
gacatctccg ccgtgccgca gtccatcgac tggcgcgact acggcgccgt gacctccgtg      480
aagaaccaga acccgtgcgg cgcctgctgg gccttcgccg ccatcgccac cgtggagtcc      540
atctacaaga tcaagaaggg catcctcgag ccgctctccg agcagcaggt gctcgactgc      600
gccaagggtc acggctgcaa gggcggctgg gagttccgcg ccttcgagtt catcatctcc      660
aacaaggggc tggcctccgg cgccatctac ccgtacaagg ccgccaaggg cacctgcaag      720
accgacggcg tgccgaactc cgcctacatc accggctacg cccgcgtgcc gcgcaacaac      780
gagtcctcca tgatgtacgc cgtgtccaag cagccgatca ccgtggccgt ggacgccaac      840
gccaacttcc agtactacaa gtccggcggtg ttcaacggcc cgtgcggcac ctccctcaac      900
cacgccgtga ccgccatcgg ctacggccag gactccatca tctaccgaa gaagtggggc      960
gccaagtggg gcgaggccgg ctacatccgc atggcccgcg acgtgtcctc ctctccgggc     1020
atctgcggca tcgccatcga cccgctctac ccgaccctcg aggagtag                       1068

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```

<210> 79
<211> 1497
<212> DNA
<213> Trichoderma reesei

```

```

<220>
<221> CDS
<222> (1)..(1497)
<223> Trichoderma reesei cellobiohydrolase I

```

```

<400> 79
atg cag tgc gcg tgt act ctc caa tgc gag act cac ccg cct ctg aca      48
Met Gln Ser Ala Cys Thr Leu Gln Ser Glu Thr His Pro Pro Leu Thr
1          5          10          15

tgg cag aaa tgc tgc tct ggt ggc acg tgc act caa cag aca ggc tcc      96
Trp Gln Lys Cys Ser Ser Gly Gly Thr Cys Thr Gln Gln Thr Gly Ser
20          25          30

```

gtg gtc atc gac gcc aac tgg cgc tgg act cac gct acg aac agc agc Val Val Ile Asp Ala Asn Trp Arg Trp Thr His Ala Thr Asn Ser Ser	144
35 40 45	
acg aac tgc tac gat ggc aac act tgg agc tcg acc cta tgt cct gac Thr Asn Cys Tyr Asp Gly Asn Thr Trp Ser Ser Thr Leu Cys Pro Asp	192
50 55 60	
aac gag acc tgc gcg aag aac tgc tgt ctg gac ggt gcc gcc tac gcg Asn Glu Thr Cys Ala Lys Asn Cys Cys Leu Asp Gly Ala Ala Tyr Ala	240
65 70 75 80	
tcc acg tac gga gtt acc acg agc ggt aac agc ctc tcc att ggc ttt Ser Thr Tyr Gly Val Thr Thr Ser Gly Asn Ser Leu Ser Ile Gly Phe	288
85 90 95	
gtc acc cag tct gcg cag aag aac gtt ggc gct cgc ctt tac ctt atg Val Thr Gln Ser Ala Gln Lys Asn Val Gly Ala Arg Leu Tyr Leu Met	336
100 105 110	
gcg agc gac acg acc tac cag gaa ttc acc ctg ctt ggc aac gag ttc Ala Ser Asp Thr Thr Tyr Gln Glu Phe Thr Leu Leu Gly Asn Glu Phe	384
115 120 125	
tct ttc gat gtt gat gtt tgc cag ctg ccg tgc ggc ttg aac gga gct Ser Phe Asp Val Asp Val Ser Gln Leu Pro Cys Gly Leu Asn Gly Ala	432
130 135 140	
ctc tac ttc gtg tcc atg gac gcg gat ggt ggc gtg agc aag tat ccc Leu Tyr Phe Val Ser Met Asp Ala Asp Gly Gly Val Ser Lys Tyr Pro	480
145 150 155 160	
acc aac acc gct ggc gcc aag tac ggc acg ggg tac tgt gac agc cag Thr Asn Thr Ala Gly Ala Lys Tyr Gly Thr Gly Tyr Cys Asp Ser Gln	528
165 170 175	
tgt ccc cgc gat ctg aag ttc atc aat ggc cag gcc aac gtt gag ggc Cys Pro Arg Asp Leu Lys Phe Ile Asn Gly Gln Ala Asn Val Glu Gly	576
180 185 190	
tgg gag ccg tca tcc aac aac gcg aac acg ggc att gga gga cac gga Trp Glu Pro Ser Ser Asn Asn Ala Asn Thr Gly Ile Gly Gly His Gly	624
195 200 205	
agc tgc tgc tct gag atg gat atc tgg gag gcc aac tcc atc tcc gag Ser Cys Cys Ser Glu Met Asp Ile Trp Glu Ala Asn Ser Ile Ser Glu	672
210 215 220	
gct ctt acc ccc cac cct tgc acg act gtc ggc cag gag atc tgc gag Ala Leu Thr Pro His Pro Cys Thr Thr Val Gly Gln Glu Ile Cys Glu	720
225 230 235 240	
ggg gat ggc tgc ggc gga act tac tcc gat aac aga tat ggc ggc act Gly Asp Gly Cys Gly Gly Thr Tyr Ser Asp Asn Arg Tyr Gly Gly Thr	768
245 250 255	
tgc gat ccc gat ggc tgc gac tgg aac cca tac cgc ctg ggc aac acc Cys Asp Pro Asp Gly Cys Asp Trp Asn Pro Tyr Arg Leu Gly Asn Thr	816

260							265							270							
agc	ttc	tac	ggc	cct	ggc	tct	agc	ttt	acc	ctc	gat	acc	acc	aag	aaa						864
Ser	Phe	Tyr	Gly	Pro	Gly	Ser	Ser	Phe	Thr	Leu	Asp	Thr	Thr	Lys	Lys						
		275						280					285								
ttg	acc	gtt	gtc	acc	cag	ttc	gag	acg	tcg	ggc	gcc	atc	aac	cga	tac						912
Leu	Thr	Val	Val	Thr	Gln	Phe	Glu	Thr	Ser	Gly	Ala	Ile	Asn	Arg	Tyr						
		290						295					300								
tat	gtc	cag	aat	ggc	gtc	act	ttc	cag	cag	ccc	aac	gcc	gag	ctt	ggc						960
Tyr	Val	Gln	Asn	Gly	Val	Thr	Phe	Gln	Gln	Pro	Asn	Ala	Glu	Leu	Gly						
		305				310				315					320						
agt	tac	tct	ggc	aac	gag	ctc	aac	gat	gat	tac	tgc	aca	gct	gag	gag						1008
Ser	Tyr	Ser	Gly	Asn	Glu	Leu	Asn	Asp	Asp	Tyr	Cys	Thr	Ala	Glu	Glu						
				325					330					335							
gca	gaa	ttc	ggc	gga	tcc	tct	ttc	tca	gac	aag	ggc	ggc	ctg	act	cag						1056
Ala	Glu	Phe	Gly	Gly	Ser	Ser	Phe	Ser	Asp	Lys	Gly	Gly	Leu	Thr	Gln						
			340					345					350								
ttc	aag	aag	gct	acc	tct	ggc	ggc	atg	gtt	ctg	gtc	atg	agt	ctg	tgg						1104
Phe	Lys	Lys	Ala	Thr	Ser	Gly	Gly	Met	Val	Leu	Val	Met	Ser	Leu	Trp						
		355						360					365								
gat	gat	tac	tac	gcc	aac	atg	ctg	tgg	ctg	gac	tcc	acc	tac	ccg	aca						1152
Asp	Asp	Tyr	Tyr	Ala	Asn	Met	Leu	Trp	Leu	Asp	Ser	Thr	Tyr	Pro	Thr						
		370				375						380									
aac	gag	acc	tcc	tcc	aca	ccc	ggc	gcc	gtg	cgc	gga	agc	tgc	tcc	acc						1200
Asn	Glu	Thr	Ser	Ser	Thr	Pro	Gly	Ala	Val	Arg	Gly	Ser	Cys	Ser	Thr						
					390					395				400							
agc	tcc	ggc	gtc	cct	gct	cag	gtc	gaa	tct	cag	tct	ccc	aac	gcc	aag						1248
Ser	Ser	Gly	Val	Pro	Ala	Gln	Val	Glu	Ser	Gln	Ser	Pro	Asn	Ala	Lys						
				405				410						415							
gtc	acc	ttc	tcc	aac	atc	aag	ttc	gga	ccc	att	ggc	agc	acc	ggc	aac						1296
Val	Thr	Phe	Ser	Asn	Ile	Lys	Phe	Gly	Pro	Ile	Gly	Ser	Thr	Gly	Asn						
				420				425					430								
cct	agc	ggc	ggc	aac	cct	ccc	ggc	gga	aac	ccg	cct	ggc	acc	acc	acc						1344
Pro	Ser	Gly	Gly	Asn	Pro	Pro	Gly	Gly	Asn	Pro	Pro	Gly	Thr	Thr	Thr						
		435						440				445									
acc	cgc	cgc	cca	gcc	act	acc	act	gga	agc	tct	ccc	gga	cct	acc	cag						1392
Thr	Arg	Arg	Pro	Ala	Thr	Thr	Thr	Gly	Ser	Ser	Pro	Gly	Pro	Thr	Gln						
				450		455					460										
tct	cac	tac	ggc	cag	tgc	ggc	ggc	att	ggc	tac	agc	ggc	ccc	acg	gtc						1440
Ser	His	Tyr	Gly	Gln	Cys	Gly	Gly	Ile	Gly	Tyr	Ser	Gly	Pro	Thr	Val						
					470					475					480						
tgc	gcc	agc	ggc	aca	act	tgc	cag	gtc	ctg	aac	cct	tac	tac	tct	cag						1488
Cys	Ala	Ser	Gly	Thr	Thr	Cys	Gln	Val	Leu	Asn	Pro	Tyr	Tyr	Ser	Gln						
				485					490					495							

tgc ctg taa
Cys Leu

1497

<210> 80
<211> 498
<212> PRT
<213> Trichoderma reesei

<400> 80

Met Gln Ser Ala Cys Thr Leu Gln Ser Glu Thr His Pro Pro Leu Thr
1 5 10 15

Trp Gln Lys Cys Ser Ser Gly Gly Thr Cys Thr Gln Gln Thr Gly Ser
20 25 30

Val Val Ile Asp Ala Asn Trp Arg Trp Thr His Ala Thr Asn Ser Ser
35 40 45

Thr Asn Cys Tyr Asp Gly Asn Thr Trp Ser Ser Thr Leu Cys Pro Asp
50 55 60

Asn Glu Thr Cys Ala Lys Asn Cys Cys Leu Asp Gly Ala Ala Tyr Ala
65 70 75 80

Ser Thr Tyr Gly Val Thr Thr Ser Gly Asn Ser Leu Ser Ile Gly Phe
85 90 95

Val Thr Gln Ser Ala Gln Lys Asn Val Gly Ala Arg Leu Tyr Leu Met
100 105 110

Ala Ser Asp Thr Thr Tyr Gln Glu Phe Thr Leu Leu Gly Asn Glu Phe
115 120 125

Ser Phe Asp Val Asp Val Ser Gln Leu Pro Cys Gly Leu Asn Gly Ala
130 135 140

Leu Tyr Phe Val Ser Met Asp Ala Asp Gly Gly Val Ser Lys Tyr Pro
145 150 155 160

Thr Asn Thr Ala Gly Ala Lys Tyr Gly Thr Gly Tyr Cys Asp Ser Gln
165 170 175

Cys Pro Arg Asp Leu Lys Phe Ile Asn Gly Gln Ala Asn Val Glu Gly
180 185 190

Trp Glu Pro Ser Ser Asn Asn Ala Asn Thr Gly Ile Gly Gly His Gly
 195 200 205

Ser Cys Cys Ser Glu Met Asp Ile Trp Glu Ala Asn Ser Ile Ser Glu
 210 215 220

Ala Leu Thr Pro His Pro Cys Thr Thr Val Gly Gln Glu Ile Cys Glu
 225 230 235 240

Gly Asp Gly Cys Gly Gly Thr Tyr Ser Asp Asn Arg Tyr Gly Gly Thr
 245 250 255

Cys Asp Pro Asp Gly Cys Asp Trp Asn Pro Tyr Arg Leu Gly Asn Thr
 260 265 270

Ser Phe Tyr Gly Pro Gly Ser Ser Phe Thr Leu Asp Thr Thr Lys Lys
 275 280 285

Leu Thr Val Val Thr Gln Phe Glu Thr Ser Gly Ala Ile Asn Arg Tyr
 290 295 300

Tyr Val Gln Asn Gly Val Thr Phe Gln Gln Pro Asn Ala Glu Leu Gly
 305 310 315 320

Ser Tyr Ser Gly Asn Glu Leu Asn Asp Asp Tyr Cys Thr Ala Glu Glu
 325 330 335

Ala Glu Phe Gly Gly Ser Ser Phe Ser Asp Lys Gly Gly Leu Thr Gln
 340 345 350

Phe Lys Lys Ala Thr Ser Gly Gly Met Val Leu Val Met Ser Leu Trp
 355 360 365

Asp Asp Tyr Tyr Ala Asn Met Leu Trp Leu Asp Ser Thr Tyr Pro Thr
 370 375 380

Asn Glu Thr Ser Ser Thr Pro Gly Ala Val Arg Gly Ser Cys Ser Thr
 385 390 395 400

Ser Ser Gly Val Pro Ala Gln Val Glu Ser Gln Ser Pro Asn Ala Lys
 405 410 415

Val Thr Phe Ser Asn Ile Lys Phe Gly Pro Ile Gly Ser Thr Gly Asn
 420 425 430

Pro Ser Gly Gly Asn Pro Pro Gly Gly Asn Pro Pro Gly Thr Thr Thr
 435 440 445

Thr Arg Arg Pro Ala Thr Thr Thr Gly Ser Ser Pro Gly Pro Thr Gln
 450 455 460

Ser His Tyr Gly Gln Cys Gly Gly Ile Gly Tyr Ser Gly Pro Thr Val
 465 470 475 480

Cys Ala Ser Gly Thr Thr Cys Gln Val Leu Asn Pro Tyr Tyr Ser Gln
 485 490 495

Cys Leu

<210> 81
 <211> 1365
 <212> DNA
 <213> *Trichoderma reesei*

<220>
 <221> CDS
 <222> (1)..(1365)
 <223> *trichoderma reesei* cellobiohydrolase II

<400> 81
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 Met Val Pro Leu Glu Arg Gln Ala Cys Ser Ser Val Trp Gly Gln
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tgt ggt ggc cag aat tgg tcg ggt ccg act tgc tgt gct tcc gga agc 96
 Cys Gly Gly Gln Asn Trp Ser Gly Pro Thr Cys Cys Ala Ser Gly Ser
 20 25 30

aca tgc gtc tac tcc aac gac tat tac tcc cag tgt ctt ccc ggc gct 144
 Thr Cys Val Tyr Ser Asn Asp Tyr Tyr Ser Gln Cys Leu Pro Gly Ala
 35 40 45

gca agc tca agc tcg tcc acg cgc gcc gcg tcg acg act tca cga gta 192
 Ala Ser Ser Ser Ser Ser Thr Arg Ala Ala Ser Thr Thr Ser Arg Val
 50 55 60

tcc ccc aca aca tcc cgg tcg agc tcc gcg acg cct cca cct ggt tct 240
 Ser Pro Thr Thr Ser Arg Ser Ser Ala Thr Pro Pro Pro Gly Ser
 65 70 75 80

acc act acc aga gta cct cca gtc gga tcg gga acc gct acg tat tca 288
 Thr Thr Thr Arg Val Pro Pro Val Gly Ser Gly Thr Ala Thr Tyr Ser

85										90					95					
ggc	aac	cct	ttt	gtt	ggg	gtc	act	cct	tgg	gcc	aat	gca	tat	tac	gcc	336				
Gly	Asn	Pro	Phe	Val	Gly	Val	Thr	Pro	Trp	Ala	Asn	Ala	Tyr	Tyr	Ala					
			100					105					110							
tct	gaa	gtt	agc	agc	ctc	gct	att	cct	agc	ttg	act	gga	gcc	atg	gcc	384				
Ser	Glu	Val	Ser	Ser	Leu	Ala	Ile	Pro	Ser	Leu	Thr	Gly	Ala	Met	Ala					
		115					120					125								
act	gct	gca	gca	gct	gtc	gca	aag	gtt	ccc	tct	ttt	atg	tgg	cta	gat	432				
Thr	Ala	Ala	Ala	Ala	Val	Ala	Lys	Val	Pro	Ser	Phe	Met	Trp	Leu	Asp					
	130					135					140									
act	ctt	gac	aag	acc	cct	ctc	atg	gag	caa	acc	ttg	gcc	gac	atc	cgc	480				
Thr	Leu	Asp	Lys	Thr	Pro	Leu	Met	Glu	Gln	Thr	Leu	Ala	Asp	Ile	Arg					
	145				150					155					160					
acc	gcc	aac	aag	aat	ggc	ggg	aac	tat	gcc	gga	cag	ttt	gtg	gtg	tat	528				
Thr	Ala	Asn	Lys	Asn	Gly	Gly	Asn	Tyr	Ala	Gly	Gln	Phe	Val	Val	Tyr					
			165						170				175							
gac	ttg	ccg	gat	cgc	gat	tgc	gct	gcc	ctt	gcc	tcg	aat	ggc	gaa	tac	576				
Asp	Leu	Pro	Asp	Arg	Asp	Cys	Ala	Ala	Leu	Ala	Ser	Asn	Gly	Glu	Tyr					
		180						185					190							
tct	att	gcc	gat	ggg	ggc	gtc	gcc	aaa	tat	aag	aac	tat	atc	gac	acc	624				
Ser	Ile	Ala	Asp	Gly	Gly	Val	Ala	Lys	Tyr	Lys	Asn	Tyr	Ile	Asp	Thr					
	195					200						205								
att	cgt	caa	att	gtc	gtg	gaa	tat	tcc	gat	atc	cgg	acc	ctc	ctg	gtt	672				
Ile	Arg	Gln	Ile	Val	Val	Glu	Tyr	Ser	Asp	Ile	Arg	Thr	Leu	Leu	Val					
	210				215						220									
att	gag	cct	gac	tct	ctt	gcc	aac	ctg	gtg	acc	aac	ctc	ggg	act	cca	720				
Ile	Glu	Pro	Asp	Ser	Leu	Ala	Asn	Leu	Val	Thr	Asn	Leu	Gly	Thr	Pro					
	225				230					235					240					
aag	tgt	gcc	aat	gct	cag	tca	gcc	tac	ctt	gag	tgc	atc	aac	tac	gcc	768				
Lys	Cys	Ala	Asn	Ala	Gln	Ser	Ala	Tyr	Leu	Glu	Cys	Ile	Asn	Tyr	Ala					
			245						250					255						
gtc	aca	cag	ctg	aac	ctt	cca	aat	gtt	gcg	atg	tat	ttg	gac	gct	ggc	816				
Val	Thr	Gln	Leu	Asn	Leu	Pro	Asn	Val	Ala	Met	Tyr	Leu	Asp	Ala	Gly					
		260						265					270							
cat	gca	gga	tgg	ctt	ggc	tgg	ccg	gca	aac	caa	gac	ccg	gcc	gct	cag	864				
His	Ala	Gly	Trp	Leu	Gly	Trp	Pro	Ala	Asn	Gln	Asp	Pro	Ala	Ala	Gln					
		275					280					285								
cta	ttt	gca	aat	gtt	tac	aag	aat	gca	tcg	tct	ccg	aga	gct	ctt	cgc	912				
Leu	Phe	Ala	Asn	Val	Tyr	Lys	Asn	Ala	Ser	Ser	Pro	Arg	Ala	Leu	Arg					
	290					295					300									
gga	ttg	gca	acc	aat	gtc	gcc	aac	tac	aac	ggg	tgg	aac	att	acc	agc	960				
Gly	Leu	Ala	Thr	Asn	Val	Ala	Asn	Tyr	Asn	Gly	Trp	Asn	Ile	Thr	Ser					
	305				310					315					320					

ccc cca tcg tac acg caa ggc aac gct gtc tac aac gag aag ctg tac 1008
 Pro Pro Ser Tyr Thr Gln Gly Asn Ala Val Tyr Asn Glu Lys Leu Tyr
 325 330 335
 atc cac gct att gga cct ctt ctt gcc aat cac ggc tgg tcc aac gcc 1056
 Ile His Ala Ile Gly Pro Leu Leu Ala Asn His Gly Trp Ser Asn Ala
 340 345 350
 ttc ttc atc act gat caa ggt cga tcg gga aag cag cct acc gga cag 1104
 Phe Phe Ile Thr Asp Gln Gly Arg Ser Gly Lys Gln Pro Thr Gly Gln
 355 360 365
 caa cag tgg gga gac tgg tgc aat gtg atc ggc acc gga ttt ggt att 1152
 Gln Gln Trp Gly Asp Trp Cys Asn Val Ile Gly Thr Gly Phe Gly Ile
 370 375 380
 cgc cca tcc gca aac act ggg gac tcg ttg ctg gat tcg ttt gtc tgg 1200
 Arg Pro Ser Ala Asn Thr Gly Asp Ser Leu Leu Asp Ser Phe Val Trp
 385 390 395 400
 gtc aag cca ggc ggc gag tgt gac ggc acc agc gac agc agt gcg cca 1248
 Val Lys Pro Gly Gly Glu Cys Asp Gly Thr Ser Asp Ser Ser Ala Pro
 405 410 415
 cga ttt gac tcc cac tgt gcg ctc cca gat gcc ttg caa ccg gcg cct 1296
 Arg Phe Asp Ser His Cys Ala Leu Pro Asp Ala Leu Gln Pro Ala Pro
 420 425 430
 caa gct ggt gct tgg ttc caa gcc tac ttt gtg cag ctt ctc aca aac 1344
 Gln Ala Gly Ala Trp Phe Gln Ala Tyr Phe Val Gln Leu Leu Thr Asn
 435 440 445
 gca aac cca tcg ttc ctg tag 1365
 Ala Asn Pro Ser Phe Leu
 450

<210> 82
 <211> 454
 <212> PRT
 <213> Trichoderma reesei

<400> 82

Met Val Pro Leu Glu Glu Arg Gln Ala Cys Ser Ser Val Trp Gly Gln
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 Cys Gly Gly Gln Asn Trp Ser Gly Pro Thr Cys Cys Ala Ser Gly Ser
 20 25 30
 Thr Cys Val Tyr Ser Asn Asp Tyr Tyr Ser Gln Cys Leu Pro Gly Ala
 35 40 45
 Ala Ser Ser Ser Ser Ser Thr Arg Ala Ala Ser Thr Thr Ser Arg Val
 50 55 60

Ser Pro Thr Thr Ser Arg Ser Ser Ser Ala Thr Pro Pro Pro Gly Ser
 65 70 75 80
 Thr Thr Thr Arg Val Pro Pro Val Gly Ser Gly Thr Ala Thr Tyr Ser
 85 90 95
 Gly Asn Pro Phe Val Gly Val Thr Pro Trp Ala Asn Ala Tyr Tyr Ala
 100 105 110
 Ser Glu Val Ser Ser Leu Ala Ile Pro Ser Leu Thr Gly Ala Met Ala
 115 120 125
 Thr Ala Ala Ala Ala Val Ala Lys Val Pro Ser Phe Met Trp Leu Asp
 130 135 140
 Thr Leu Asp Lys Thr Pro Leu Met Glu Gln Thr Leu Ala Asp Ile Arg
 145 150 155 160
 Thr Ala Asn Lys Asn Gly Gly Asn Tyr Ala Gly Gln Phe Val Val Tyr
 165 170 175
 Asp Leu Pro Asp Arg Asp Cys Ala Ala Leu Ala Ser Asn Gly Glu Tyr
 180 185 190
 Ser Ile Ala Asp Gly Gly Val Ala Lys Tyr Lys Asn Tyr Ile Asp Thr
 195 200 205
 Ile Arg Gln Ile Val Val Glu Tyr Ser Asp Ile Arg Thr Leu Leu Val
 210 215 220
 Ile Glu Pro Asp Ser Leu Ala Asn Leu Val Thr Asn Leu Gly Thr Pro
 225 230 235 240
 Lys Cys Ala Asn Ala Gln Ser Ala Tyr Leu Glu Cys Ile Asn Tyr Ala
 245 250 255
 Val Thr Gln Leu Asn Leu Pro Asn Val Ala Met Tyr Leu Asp Ala Gly
 260 265 270
 His Ala Gly Trp Leu Gly Trp Pro Ala Asn Gln Asp Pro Ala Ala Gln
 275 280 285

Leu Phe Ala Asn Val Tyr Lys Asn Ala Ser Ser Pro Arg Ala Leu Arg
 290 295 300
 Gly Leu Ala Thr Asn Val Ala Asn Tyr Asn Gly Trp Asn Ile Thr Ser
 305 310 315 320
 Pro Pro Ser Tyr Thr Gln Gly Asn Ala Val Tyr Asn Glu Lys Leu Tyr
 325 330 335
 Ile His Ala Ile Gly Pro Leu Leu Ala Asn His Gly Trp Ser Asn Ala
 340 345 350
 Phe Phe Ile Thr Asp Gln Gly Arg Ser Gly Lys Gln Pro Thr Gly Gln
 355 360 365
 Gln Gln Trp Gly Asp Trp Cys Asn Val Ile Gly Thr Gly Phe Gly Ile
 370 375 380
 Arg Pro Ser Ala Asn Thr Gly Asp Ser Leu Leu Asp Ser Phe Val Trp
 385 390 395 400
 Val Lys Pro Gly Gly Glu Cys Asp Gly Thr Ser Asp Ser Ser Ala Pro
 405 410 415
 Arg Phe Asp Ser His Cys Ala Leu Pro Asp Ala Leu Gln Pro Ala Pro
 420 425 430
 Gln Ala Gly Ala Trp Phe Gln Ala Tyr Phe Val Gln Leu Leu Thr Asn
 435 440 445
 Ala Asn Pro Ser Phe Leu
 450

<210> 83
 <211> 1317
 <212> DNA
 <213> Trichoderma reesei

<220>
 <221> CDS
 <222> (1)..(1317)
 <223> Trichoderma reesei endoglucanase I

<400> 83
 atg cag caa ccg gga acc agc acc ccc gag gtc cat ccc aag ttg aca
 Met Gln Gln Pro Gly Thr Ser Thr Pro Glu Val His Pro Lys Leu Thr

48

1	5	10	15	
acc tac aag tgc	aca aag tcc ggg	ggg tgc gtg gcc	cag gac acc tcg	96
Thr Tyr Lys Cys	Thr Lys Ser Gly	Gly Cys Val Ala	Gln Asp Thr Ser	
20		25	30	
gtg gtc ctt gac	tgg aac tac cgc	tgg atg cac gac	gca aac tac aac	144
Val Val Leu Asp	Trp Asn Tyr Arg	Trp Met His Asp	Ala Asn Tyr Asn	
35	40	45		
tcg tgc acc gtc	aac ggc ggc gtc	aac acc acg ctc	tgc cct gac gag	192
Ser Cys Thr Val	Asn Gly Gly Val	Asn Thr Thr Leu	Cys Pro Asp Glu	
50	55	60		
gcg acc tgt ggc	aag aac tgc ttc	atc gag ggc gtc	gac tac gcc gcc	240
Ala Thr Cys Gly	Lys Asn Cys Phe	Ile Glu Gly Val	Asp Tyr Ala Ala	
65	70	75	80	
tcg ggc gtc acg	acc tgc ggc agc	agc ctc acc atg	aac cag tac atg	288
Ser Gly Val Thr	Thr Ser Gly Ser	Ser Ser Leu Thr	Met Asn Gln Tyr	
85	90	95		
ccc agc agc tct	ggc ggc tac agc	agc gtc tct cct	cgg ctg tat ctc	336
Pro Ser Ser Ser	Gly Gly Tyr Ser	Ser Val Ser Pro	Arg Leu Tyr Leu	
100	105	110		
ctg gac tct gac	ggc gag tac gtg	atg ctg aag ctc	aac ggc cag gag	384
Leu Asp Ser Asp	Gly Glu Tyr Val	Met Leu Lys Leu	Asn Gly Gln Glu	
115	120	125		
ctg agc ttc gac	gtc gac ctc tct	gct ctg ccg tgt	gga gag aac ggc	432
Leu Ser Phe Asp	Val Asp Leu Ser	Ala Leu Pro Cys	Gly Glu Asn Gly	
130	135	140		
tcg ctc tac ctg	tct cag atg gac	gag aac ggg ggc	gcc aac cag tat	480
Ser Leu Tyr Leu	Ser Gln Met Asp	Glu Asn Gly Gly	Ala Asn Gln Tyr	
145	150	155	160	
aac acg gcc ggt	gcc aac tac ggg	agc ggc tac tgc	gat gct cag tgc	528
Asn Thr Ala Gly	Ala Asn Tyr Gly	Ser Gly Tyr Cys	Asp Ala Gln Cys	
165	170	175		
ccc gtc cag aca	tgg agg aac ggc	acc ctc aac act	agc cac cag gcc	576
Pro Val Gln Thr	Trp Arg Asn Gly	Thr Leu Asn Thr	Ser His Gln Gly	
180	185	190		
ttc tgc tgc aac	gag atg gat atc	ctg gag ggc aac	tcg agg gcg aat	624
Phe Cys Cys Asn	Glu Met Asp Ile	Leu Glu Gly Asn	Ser Arg Ala Asn	
195	200	205		
gcc ttg acc cct	cac tct tgc acg	gcc acg gcc tgc	gac tct gcc ggt	672
Ala Leu Thr Pro	His Ser Cys Thr	Ala Thr Ala Cys	Asp Ser Ala Gly	
210	215	220		
tgc ggc ttc aac	ccc tat ggc agc	ggc tac aaa agc	tac tac ggc ccc	720
Cys Gly Phe Asn	Pro Tyr Gly Ser	Gly Tyr Lys Ser	Tyr Tyr Gly Pro	
225	230	235	240	

gga gat acc gtt gac acc tcc aag acc ttc acc atc atc acc cag ttc 768
 Gly Asp Thr Val Asp Thr Ser Lys Thr Phe Thr Ile Ile Thr Gln Phe
 245 250 255

aac acg gac aac ggc tcg ccc tcg ggc aac ctt gtg agc atc acc cgc 816
 Asn Thr Asp Asn Gly Ser Pro Ser Gly Asn Leu Val Ser Ile Thr Arg
 260 265 270

aag tac cag caa aac ggc gtc gac atc ccc agc gcc cag ccc ggc ggc 864
 Lys Tyr Gln Gln Asn Gly Val Asp Ile Pro Ser Ala Gln Pro Gly Gly
 275 280 285

gac acc atc tcg tcc tgc ccg tcc gcc tca gcc tac ggc ggc ctc gcc 912
 Asp Thr Ile Ser Ser Cys Pro Ser Ala Ser Ala Tyr Gly Gly Leu Ala
 290 295 300

acc atg ggc aag gcc ctg agc agc ggc atg gtg ctc gtg ttc agc att 960
 Thr Met Gly Lys Ala Leu Ser Ser Gly Met Val Leu Val Phe Ser Ile
 305 310 315 320

tgg aac gac aac agc cag tac atg aac tgg ctc gac agc ggc aac gcc 1008
 Trp Asn Asp Asn Ser Gln Tyr Met Asn Trp Leu Asp Ser Gly Asn Ala
 325 330 335

ggc ccc tgc agc agc acc gag ggc aac cca tcc aac acc ctg gcc aac 1056
 Gly Pro Cys Ser Ser Thr Glu Gly Asn Pro Ser Asn Thr Leu Ala Asn
 340 345 350

aac ccc aac acg cac gtc gtc ttc tcc aac atc cgc tgg gga gac att 1104
 Asn Pro Asn Thr His Val Val Phe Ser Asn Ile Arg Trp Gly Asp Ile
 355 360 365

ggg tct act acg aac tcg act gcg ccc ccg ccc ccg cct gcg tcc agc 1152
 Gly Ser Thr Thr Asn Ser Thr Ala Pro Pro Pro Pro Pro Ala Ser Ser
 370 375 380

acg acg ttt tcg act aca cgg agg agc tcg acg act tcg agc agc ccg 1200
 Thr Thr Phe Ser Thr Thr Arg Arg Ser Ser Thr Thr Ser Ser Ser Pro
 385 390 395 400

agc tgc acg cag act cac tgg ggg cag tgc ggt ggc att ggg tac agc 1248
 Ser Cys Thr Gln Thr His Trp Gly Gln Cys Gly Gly Ile Gly Tyr Ser
 405 410 415

ggg tgc aag acg tgc acg tcg ggc act acg tgc cag tat agc aac gac 1296
 Gly Cys Lys Thr Cys Thr Ser Gly Thr Thr Cys Gln Tyr Ser Asn Asp
 420 425 430

tac tac tcg caa tgc ctt tag 1317
 Tyr Tyr Ser Gln Cys Leu
 435

<210> 84
 <211> 438
 <212> PRT
 <213> Trichoderma reesei

<400> 84

Met Gln Gln Pro Gly Thr Ser Thr Pro Glu Val His Pro Lys Leu Thr
 1 5 10 15

Thr Tyr Lys Cys Thr Lys Ser Gly Gly Cys Val Ala Gln Asp Thr Ser
 20 25 30

Val Val Leu Asp Trp Asn Tyr Arg Trp Met His Asp Ala Asn Tyr Asn
 35 40 45

Ser Cys Thr Val Asn Gly Gly Val Asn Thr Thr Leu Cys Pro Asp Glu
 50 55 60

Ala Thr Cys Gly Lys Asn Cys Phe Ile Glu Gly Val Asp Tyr Ala Ala
 65 70 75 80

Ser Gly Val Thr Thr Ser Gly Ser Ser Leu Thr Met Asn Gln Tyr Met
 85 90 95

Pro Ser Ser Ser Gly Gly Tyr Ser Ser Val Ser Pro Arg Leu Tyr Leu
 100 105 110

Leu Asp Ser Asp Gly Glu Tyr Val Met Leu Lys Leu Asn Gly Gln Glu
 115 120 125

Leu Ser Phe Asp Val Asp Leu Ser Ala Leu Pro Cys Gly Glu Asn Gly
 130 135 140

Ser Leu Tyr Leu Ser Gln Met Asp Glu Asn Gly Gly Ala Asn Gln Tyr
 145 150 155 160

Asn Thr Ala Gly Ala Asn Tyr Gly Ser Gly Tyr Cys Asp Ala Gln Cys
 165 170 175

Pro Val Gln Thr Trp Arg Asn Gly Thr Leu Asn Thr Ser His Gln Gly
 180 185 190

Phe Cys Cys Asn Glu Met Asp Ile Leu Glu Gly Asn Ser Arg Ala Asn
 195 200 205

Ala Leu Thr Pro His Ser Cys Thr Ala Thr Ala Cys Asp Ser Ala Gly
 210 215 220

Cys Gly Phe Asn Pro Tyr Gly Ser Gly Tyr Lys Ser Tyr Tyr Gly Pro
 225 230 235 240

Gly Asp Thr Val Asp Thr Ser Lys Thr Phe Thr Ile Ile Thr Gln Phe
 245 250 255

Asn Thr Asp Asn Gly Ser Pro Ser Gly Asn Leu Val Ser Ile Thr Arg
 260 265 270

Lys Tyr Gln Gln Asn Gly Val Asp Ile Pro Ser Ala Gln Pro Gly Gly
 275 280 285

Asp Thr Ile Ser Ser Cys Pro Ser Ala Ser Ala Tyr Gly Gly Leu Ala
 290 295 300

Thr Met Gly Lys Ala Leu Ser Ser Gly Met Val Leu Val Phe Ser Ile
 305 310 315 320

Trp Asn Asp Asn Ser Gln Tyr Met Asn Trp Leu Asp Ser Gly Asn Ala
 325 330 335

Gly Pro Cys Ser Ser Thr Glu Gly Asn Pro Ser Asn Thr Leu Ala Asn
 340 345 350

Asn Pro Asn Thr His Val Val Phe Ser Asn Ile Arg Trp Gly Asp Ile
 355 360 365

Gly Ser Thr Thr Asn Ser Thr Ala Pro Pro Pro Pro Pro Ala Ser Ser
 370 375 380

Thr Thr Phe Ser Thr Thr Arg Arg Ser Ser Thr Thr Ser Ser Ser Pro
 385 390 395 400

Ser Cys Thr Gln Thr His Trp Gly Gln Cys Gly Gly Ile Gly Tyr Ser
 405 410 415

Gly Cys Lys Thr Cys Thr Ser Gly Thr Thr Cys Gln Tyr Ser Asn Asp
 420 425 430

Tyr Tyr Ser Gln Cys Leu
 435

<210> 85
 <211> 954

<212> DNA
 <213> Artificial Sequence

<220>
 <223> 6GP1

<220>
 <221> CDS
 <222> (1)..(954)
 <223> 6GP1

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<400> 85
atg ggc gtg gac ccg ttc gag cgc aac aag atc ctc ggc cgc ggc atc      48
Met Gly Val Asp Pro Phe Glu Arg Asn Lys Ile Leu Gly Arg Gly Ile
1          5          10          15

aac atc ggc aac gcc ctg gag gcc ccg aac gag ggc gac tgg ggc gtg      96
Asn Ile Gly Asn Ala Leu Glu Ala Pro Asn Glu Gly Asp Trp Gly Val
          20          25          30

gtg atc aag gac gag ttc ttc gac atc atc aag gag gcc ggc ttc tcc      144
Val Ile Lys Asp Glu Phe Phe Asp Ile Ile Lys Glu Ala Gly Phe Ser
          35          40          45

cac gtg cgc atc ccg atc cgc tgg tcc acc cac gcc tac gcc ttc ccg      192
His Val Arg Ile Pro Ile Arg Trp Ser Thr His Ala Tyr Ala Phe Pro
          50          55          60

ccg tac aag atc atg gac cgc ttc ttc aag cgc gtg gac gag gtg atc      240
Pro Tyr Lys Ile Met Asp Arg Phe Phe Lys Arg Val Asp Glu Val Ile
65          70          75          80

aac ggc gcc ctc aag cgc gcc ctc gcc gtg gcc atc aac atc cac cac      288
Asn Gly Ala Leu Lys Arg Gly Leu Ala Val Ala Ile Asn Ile His His
          85          90          95

tac gag gag ctc atg aac gac ccg gag gag cac aag gag cgc ttc ctc      336
Tyr Glu Glu Leu Met Asn Asp Pro Glu Glu His Lys Glu Arg Phe Leu
          100          105          110

gcc ctc tgg aag cag atc gcc gac cgc tac aag gac tac ccg gag acc      384
Ala Leu Trp Lys Gln Ile Ala Asp Arg Tyr Lys Asp Tyr Pro Glu Thr
          115          120          125

ctc ttc ttc gag atc ctc aac gag ccg cac ggc aac ctc acc ccg gag      432
Leu Phe Phe Glu Ile Leu Asn Glu Pro His Gly Asn Leu Thr Pro Glu
          130          135          140

aag tgg aac gag ctg ctc gag gag gcc ctc aag gtg atc cgc tcc atc      480
Lys Trp Asn Glu Leu Leu Glu Glu Ala Leu Lys Val Ile Arg Ser Ile
145          150          155          160

gac aag aag cac acc atc atc att ggc acc gca gag tgg gga ggc atc      528
Asp Lys Lys His Thr Ile Ile Ile Gly Thr Ala Glu Trp Gly Gly Ile
          165          170          175

tcc gcc ctc gag aag ctc tcc gtg ccg aag tgg gag aag aat tcc atc      576

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Ser Ala Leu Glu Lys Leu Ser Val Pro Lys Trp Glu Lys Asn- Ser Ile
 180 185 190
 gtg acc atc cac tac tac aac ccg ttc gag ttc acg cac cag ggc gcc 624
 Val Thr Ile His Tyr Tyr Asn Pro Phe Glu Phe Thr His Gln Gly Ala
 195 200 205
 gag tgg gtg gag ggc tcc gag aag tgg ctt ggc cgc aag tgg ggc tcc 672
 Glu Trp Val Glu Gly Ser Glu Lys Trp Leu Gly Arg Lys Trp Gly Ser
 210 215 220
 ccg gac gac cag aag cac ctc atc gag gag ttc aac ttc atc gag gag 720
 Pro Asp Asp Gln Lys His Leu Ile Glu Glu Phe Asn Phe Ile Glu Glu
 225 230 235 240
 tgg tcc aag aag aac aag cgc ccg atc tac atc ggc gag ttt ggc gcc 768
 Trp Ser Lys Lys Asn Lys Arg Pro Ile Tyr Ile Gly Glu Phe Gly Ala
 245 250 255
 tac cgc aag gcc gac ctc gag tcc cgc atc aag tgg acc tcc ttc gtg 816
 Tyr Arg Lys Ala Asp Leu Glu Ser Arg Ile Lys Trp Thr Ser Phe Val
 260 265 270
 gtg cgt gag atg gag aag cgc cgc tgg tcc tgg gcc tac tgg gag ttc 864
 Val Arg Glu Met Glu Lys Arg Arg Trp Ser Trp Ala Tyr Trp Glu Phe
 275 280 285
 tgc tcc ggc ttc ggc gtg tac gac acc ctc cgc aag acc tgg aac aag 912
 Cys Ser Gly Phe Gly Val Tyr Asp Thr Leu Arg Lys Thr Trp Asn Lys
 290 295 300
 gac ctc ctc gag gcc ctc atc ggc ggc gac tcc atc gag tag 954
 Asp Leu Leu Glu Ala Leu Ile Gly Gly Asp Ser Ile Glu
 305 310 315

<210> 86
 <211> 317
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 86

Met Gly Val Asp Pro Phe Glu Arg Asn Lys Ile Leu Gly Arg Gly Ile
 1 5 10 15

Asn Ile Gly Asn Ala Leu Glu Ala Pro Asn Glu Gly Asp Trp Gly Val
 20 25 30

Val Ile Lys Asp Glu Phe Phe Asp Ile Ile Lys Glu Ala Gly Phe Ser
 35 40 45

His Val Arg Ile Pro Ile Arg Trp Ser Thr His Ala Tyr Ala Phe Pro
 50 55 60

Pro Tyr Lys Ile Met Asp Arg Phe Phe Lys Arg Val Asp Glu Val Ile
 65 70 75 80

Asn Gly Ala Leu Lys Arg Gly Leu Ala Val Ala Ile Asn Ile His His
 85 90 95

Tyr Glu Glu Leu Met Asn Asp Pro Glu Glu His Lys Glu Arg Phe Leu
 100 105 110

Ala Leu Trp Lys Gln Ile Ala Asp Arg Tyr Lys Asp Tyr Pro Glu Thr
 115 120 125

Leu Phe Phe Glu Ile Leu Asn Glu Pro His Gly Asn Leu Thr Pro Glu
 130 135 140

Lys Trp Asn Glu Leu Leu Glu Glu Ala Leu Lys Val Ile Arg Ser Ile
 145 150 155 160

Asp Lys Lys His Thr Ile Ile Ile Gly Thr Ala Glu Trp Gly Gly Ile
 165 170 175

Ser Ala Leu Glu Lys Leu Ser Val Pro Lys Trp Glu Lys Asn Ser Ile
 180 185 190

Val Thr Ile His Tyr Tyr Asn Pro Phe Glu Phe Thr His Gln Gly Ala
 195 200 205

Glu Trp Val Glu Gly Ser Glu Lys Trp Leu Gly Arg Lys Trp Gly Ser
 210 215 220

Pro Asp Asp Gln Lys His Leu Ile Glu Glu Phe Asn Phe Ile Glu Glu
 225 230 235 240

Trp Ser Lys Lys Asn Lys Arg Pro Ile Tyr Ile Gly Glu Phe Gly Ala
 245 250 255

Tyr Arg Lys Ala Asp Leu Glu Ser Arg Ile Lys Trp Thr Ser Phe Val
 260 265 270

Val Arg Glu Met Glu Lys Arg Arg Trp Ser Trp Ala Tyr Trp Glu Phe
 275 280 285

Cys Ser Gly Phe Gly Val Tyr Asp Thr Leu Arg Lys Thr Trp Asn Lys
 290 295 300

Asp Leu Leu Glu Ala Leu Ile Gly Gly Asp Ser Ile Glu
 305 310 315

<210> 87
 <211> 1248
 <212> DNA
 <213> Hordeum vulgare

<220>
 <221> CDS
 <222> (1)..(1248)
 <223> Barley AmyI amylase

<400> 87
 atg gca cac caa gtc ctc ttt cag ggg ttc aac tgg gag tcg tgg aag 48
 Met Ala His Gln Val Leu Phe Gln Gly Phe Asn Trp Glu Ser Trp Lys
 1 5 10 15
 cag agc ggc ggg tgg tac aac atg atg atg ggc aag gtc gac gac atc 96
 Gln Ser Gly Gly Trp Tyr Asn Met Met Met Gly Lys Val Asp Asp Ile
 20 25 30
 gcc gct gcc gga gtc acc cac gtc tgg ctg cca ccg ccg tcg cac tcc 144
 Ala Ala Ala Gly Val Thr His Val Trp Leu Pro Pro Pro Ser His Ser
 35 40 45
 gtc tcc aac gaa ggt tac atg cct ggt cgg ctg tac gac atc gac gcg 192
 Val Ser Asn Glu Gly Tyr Met Pro Gly Arg Leu Tyr Asp Ile Asp Ala
 50 55 60
 tcc aag tac ggc aac gcg gcg gag ctc aag tcg ctc atc ggc gcg ctc 240
 Ser Lys Tyr Gly Asn Ala Ala Glu Leu Lys Ser Leu Ile Gly Ala Leu
 65 70 75 80
 cac ggc aag ggc gtg cag gcc atc gcc gac atc gtc atc aac cac cgc 288
 His Gly Lys Gly Val Gln Ala Ile Ala Asp Ile Val Ile Asn His Arg
 85 90 95
 tgc gcc gac tac aag gat agc cgc ggc atc tac tgc atc ttc gag ggc 336
 Cys Ala Asp Tyr Lys Asp Ser Arg Gly Ile Tyr Cys Ile Phe Glu Gly
 100 105 110
 ggc acc tcc gac ggc cgc ctc gac tgg ggc ccc cac atg atc tgt cgc 384
 Gly Thr Ser Asp Gly Arg Leu Asp Trp Gly Pro His Met Ile Cys Arg
 115 120 125
 gac gac acc aaa tac tcc gat ggc acc gca aac ctc gac acc gga gcc 432
 Asp Asp Thr Lys Tyr Ser Asp Gly Thr Ala Asn Leu Asp Thr Gly Ala
 130 135 140

gac ttc gcc gcc gcg ccc gac atc gac cac ctc aac gac cgg gtc cag Asp Phe Ala Ala Ala Pro Asp Ile Asp His Leu Asn Asp Arg Val Gln 145 150 155 160	480
cgc gag ctc aag gag tgg ctc ctc tgg ctc aag agc gac ctc ggc ttc Arg Glu Leu Lys Glu Trp Leu Leu Trp Leu Lys Ser Asp Leu Gly Phe 165 170 175	528
gac gcg tgg cgc ctt gac ttc gcc agg ggc tac tcg ccg gag atg gcc Asp Ala Trp Arg Leu Asp Phe Ala Arg Gly Tyr Ser Pro Glu Met Ala 180 185 190	576
aag gtg tac atc gac ggc aca tcc ccg agc ctc gcc gtg gcc gag gtg Lys Val Tyr Ile Asp Gly Thr Pro Ser Leu Ala Val Ala Glu Val 195 200 205	624
tgg gac aat atg gcc acc ggc ggc gac ggc aag ccc aac tac gac cag Trp Asp Asn Met Ala Thr Gly Gly Asp Gly Lys Pro Asn Tyr Asp Gln 210 215 220	672
gac gcg cac cgg cag aat ctg gtg aac tgg gtg gac aag gtg ggc ggc Asp Ala His Arg Gln Asn Leu Val Asn Trp Val Asp Lys Val Gly Gly 225 230 235 240	720
gcg gcc tcg gca ggc atg gtg ttc gac ttc acg acc aaa ggg ata ctg Ala Ala Ser Ala Gly Met Val Phe Asp Phe Thr Thr Lys Gly Ile Leu 245 250 255	768
aac gct gcc gtg gag ggc gag ctg tgg agg ctg atc gac ccg cag ggc Asn Ala Ala Val Glu Gly Glu Leu Trp Arg Leu Ile Asp Pro Gln Gly 260 265 270	816
aag gcc ccc ggc gtg atg gga tgg tgg ccg gcc aag gcc gtc acc ttc Lys Ala Pro Gly Val Met Gly Trp Trp Pro Ala Lys Ala Val Thr Phe 275 280 285	864
gtc gac aac cac gat aca ggc tcc acg cag gcc atg tgg cca ttc ccc Val Asp Asn His Asp Thr Gly Ser Thr Gln Ala Met Trp Pro Phe Pro 290 295 300	912
tcc gac aag gtc atg cag ggc tac gcg tac atc ctc acc cac ccc ggc Ser Asp Lys Val Met Gln Gly Tyr Ala Tyr Ile Leu Thr His Pro Gly 305 310 315 320	960
atc cca tgc atc ttc tac gac cat ttc ttc aac tgg ggg ttt aag gac Ile Pro Cys Ile Phe Tyr Asp His Phe Phe Asn Trp Gly Phe Lys Asp 325 330 335	1008
cag atc gcg gcg ctg gtg gcg atc agg aag cgc aac ggc atc acg gcg Gln Ile Ala Ala Leu Val Ala Ile Arg Lys Arg Asn Gly Ile Thr Ala 340 345 350	1056
acg agc gct ctg aag atc ctc atg cac gaa gga gat gcc tac gtc gcc Thr Ser Ala Leu Lys Ile Leu Met His Glu Gly Asp Ala Tyr Val Ala 355 360 365	1104
gag ata gac ggc aag gtg gtg gtg aag atc ggg tcc agg tac gac gtc Glu Ile Asp Gly Lys Val Val Val Lys Ile Gly Ser Arg Tyr Asp Val 370 375 380 385 390	1152

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      370              375              380
ggg gcg gtg atc ccg gcc ggg ttc gtg acc tcg gca cac ggc aac gac      1200
Gly Ala Val Ile Pro Ala Gly Phe Val Thr Ser Ala His Gly Asn Asp
385              390              395              400

tac gcc gtc tgg gag aag aac ggt gcc gcg gca aca cta caa cgg agc      1248
Tyr Ala Val Trp Glu Lys Asn Gly Ala Ala Ala Thr Leu Gln Arg Ser
              405              410              415

<210> 88
<211> 416
<212> PRT
<213> Hordeum vulgare

<400> 88

Met Ala His Gln Val Leu Phe Gln Gly Phe Asn Trp Glu Ser Trp Lys
1              5              10              15

Gln Ser Gly Gly Trp Tyr Asn Met Met Met Gly Lys Val Asp Asp Ile
20              25              30

Ala Ala Ala Gly Val Thr His Val Trp Leu Pro Pro Pro Ser His Ser
35              40              45

Val Ser Asn Glu Gly Tyr Met Pro Gly Arg Leu Tyr Asp Ile Asp Ala
50              55              60

Ser Lys Tyr Gly Asn Ala Ala Glu Leu Lys Ser Leu Ile Gly Ala Leu
65              70              75              80

His Gly Lys Gly Val Gln Ala Ile Ala Asp Ile Val Ile Asn His Arg
85              90              95

Cys Ala Asp Tyr Lys Asp Ser Arg Gly Ile Tyr Cys Ile Phe Glu Gly
100              105              110

Gly Thr Ser Asp Gly Arg Leu Asp Trp Gly Pro His Met Ile Cys Arg
115              120              125

Asp Asp Thr Lys Tyr Ser Asp Gly Thr Ala Asn Leu Asp Thr Gly Ala
130              135              140

Asp Phe Ala Ala Ala Pro Asp Ile Asp His Leu Asn Asp Arg Val Gln
145              150              155              160

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Arg Glu Leu Lys Glu Trp Leu Leu Trp Leu Lys Ser Asp Leu Gly Phe
 165 170 175

Asp Ala Trp Arg Leu Asp Phe Ala Arg Gly Tyr Ser Pro Glu Met Ala
 180 185 190

Lys Val Tyr Ile Asp Gly Thr Ser Pro Ser Leu Ala Val Ala Glu Val
 195 200 205

Trp Asp Asn Met Ala Thr Gly Gly Asp Gly Lys Pro Asn Tyr Asp Gln
 210 215 220

Asp Ala His Arg Gln Asn Leu Val Asn Trp Val Asp Lys Val Gly Gly
 225 230 235 240

Ala Ala Ser Ala Gly Met Val Phe Asp Phe Thr Thr Lys Gly Ile Leu
 245 250 255

Asn Ala Ala Val Glu Gly Glu Leu Trp Arg Leu Ile Asp Pro Gln Gly
 260 265 270

Lys Ala Pro Gly Val Met Gly Trp Trp Pro Ala Lys Ala Val Thr Phe
 275 280 285

Val Asp Asn His Asp Thr Gly Ser Thr Gln Ala Met Trp Pro Phe Pro
 290 295 300

Ser Asp Lys Val Met Gln Gly Tyr Ala Tyr Ile Leu Thr His Pro Gly
 305 310 315 320

Ile Pro Cys Ile Phe Tyr Asp His Phe Phe Asn Trp Gly Phe Lys Asp
 325 330 335

Gln Ile Ala Ala Leu Val Ala Ile Arg Lys Arg Asn Gly Ile Thr Ala
 340 345 350

Thr Ser Ala Leu Lys Ile Leu Met His Glu Gly Asp Ala Tyr Val Ala
 355 360 365

Glu Ile Asp Gly Lys Val Val Val Lys Ile Gly Ser Arg Tyr Asp Val
 370 375 380

Gly Ala Val Ile Pro Ala Gly Phe Val Thr Ser Ala His Gly Asn Asp
 385 390 395 400

Tyr Ala Val Trp Glu Lys Asn Gly Ala Ala Ala Thr Leu Gln Arg Ser
 405 410 415

<210> 89
 <211> 1401
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> *Trichoderma reesei* β -Glucosidase 2

<220>
 <221> CDS
 <222> (1)..(1401)
 <223> *Trichoderma reesei* β -Glucosidase 2

<400> 89
 atg ttg ccc aag gac ttt cag tgg ggg ttc gcc acg gct gcc tac cag 48
 Met Leu Pro Lys Asp Phe Gln Trp Gly Phe Ala Thr Ala Ala Tyr Gln
 1 5 10 15
 atc gag ggc gcc gtc gac cag gac ggc cgc ggc ccc agc atc tgg gac 96
 Ile Glu Gly Ala Val Asp Gln Asp Gly Arg Gly Pro Ser Ile Trp Asp
 20 25 30
 acg ttc tgc gcg cag ccc ggc aag atc gcc gac ggc tcg tcg ggc gtg 144
 Thr Phe Cys Ala Gln Pro Gly Lys Ile Ala Asp Gly Ser Ser Gly Val
 35 40 45
 acg gcg tgc gac tcg tac aac cgc acg gcc gag gac att gcg ctg ctg 192
 Thr Ala Cys Asp Ser Tyr Asn Arg Thr Ala Glu Asp Ile Ala Leu Leu
 50 55 60
 aag tcg ctc ggg gcc aag agc tac cgc ttc tcc atc tcg tgg tcg cgc 240
 Lys Ser Leu Gly Ala Lys Ser Tyr Arg Phe Ser Ile Ser Trp Ser Arg
 65 70 75 80
 atc atc ccc gag ggc ggc cgc ggc gat gcc gtc aac cag gcg ggc atc 288
 Ile Ile Pro Glu Gly Gly Arg Gly Asp Ala Val Asn Gln Ala Gly Ile
 85 90 95
 gac cac tac gtc aag ttc gtc gac gac ctg ctc gac gcc ggc atc acg 336
 Asp His Tyr Val Lys Phe Val Asp Asp Leu Leu Asp Ala Gly Ile Thr
 100 105 110
 ccc ttc atc acc ctc ttc cac tgg gac ctg ccc gag ggc ctg cat cag 384
 Pro Phe Ile Thr Leu Phe His Trp Asp Leu Pro Glu Gly Leu His Gln
 115 120 125
 cgg tac ggg ggg ctg ctg aac cgc acc gag ttc ccg ctc gac ttt gaa 432
 Arg Tyr Gly Gly Leu Leu Asn Arg Thr Glu Phe Pro Leu Asp Phe Glu
 130 135 140
 aac tac gcc cgc gtc atg ttc agg gcg ctg ccc aag gtg cgc aac tgg 480

Asn Tyr Ala Arg Val Met Phe Arg Ala Leu Pro Lys Val Arg Asn Trp	
145 150 155 160	
atc acc ttc aac gag ccg ctg tgc tgc gcc atc ccg ggc tac ggc tcc	528
Ile Thr Phe Asn Glu Pro Leu Cys Ser Ala Ile Pro Gly Tyr Gly Ser	
165 170 175	
ggc acc ttc gcc ccc gcc ccg cag agc acc tcg gag ccg tgg acc gtc	576
Gly Thr Phe Ala Pro Gly Arg Gln Ser Thr Ser Glu Pro Trp Thr Val	
180 185 190	
ggc cac aac atc ctc gtc gcc cac ggc cgc gcc gtc aag gcg tac cgc	624
Gly His Asn Ile Leu Val Ala His Gly Arg Ala Val Lys Ala Tyr Arg	
195 200 205	
gac gac ttc aag ccc gcc agc ggc gac ggc cag atc ggc atc gtc ctc	672
Asp Asp Phe Lys Pro Ala Ser Gly Asp Gly Gln Ile Gly Ile Val Leu	
210 215 220	
aac ggc gac ttc acc tac ccc tgg gac gcc gcc gac ccg gcc gac aag	720
Asn Gly Asp Phe Thr Tyr Pro Trp Asp Ala Ala Asp Pro Ala Asp Lys	
225 230 235 240	
gag gcg gcc gag ccg cgc ctc gag ttc ttc acg gcc tgg ttc gcg gac	768
Glu Ala Ala Glu Arg Leu Glu Phe Phe Thr Ala Trp Phe Ala Asp	
245 250 255	
ccc atc tac ttg ggc gac tac ccg gcg tcg atg cgc aag cag ctg ggc	816
Pro Ile Tyr Leu Gly Asp Tyr Pro Ala Ser Met Arg Lys Gln Leu Gly	
260 265 270	
gac ccg ctg ccg acc ttt acg ccc gag gag cgc gcc ctc gtc cac ggc	864
Asp Arg Leu Pro Thr Phe Thr Pro Glu Glu Arg Ala Leu Val His Gly	
275 280 285	
tcc aac gac ttt tac ggc atg aac cac tac acg tcc aac tac atc cgc	912
Ser Asn Asp Phe Tyr Gly Met Asn His Tyr Thr Ser Asn Tyr Ile Arg	
290 295 300	
cac cgc agc tcg ccc gcc tcc gcc gac gac acc gtc ggc aac gtc gac	960
His Arg Ser Ser Pro Ala Ser Ala Asp Asp Thr Val Gly Asn Val Asp	
305 310 315 320	
gtg ctc ttc acc aac aag cag ggc aac tgc atc ggc ccc gag acg cag	1008
Val Leu Phe Thr Asn Lys Gln Gly Asn Cys Ile Gly Pro Glu Thr Gln	
325 330 335	
tcc ccc tgg ctg cgc ccc tgt gcc gcc ggc ttc cgc gac ttc ctg gtg	1056
Ser Pro Trp Leu Arg Pro Cys Ala Ala Gly Phe Arg Asp Phe Leu Val	
340 345 350	
tgg atc agc aag agg tac ggc tac ccg ccc atc tac gtg acg gag aac	1104
Trp Ile Ser Lys Arg Tyr Gly Tyr Pro Pro Ile Tyr Val Thr Glu Asn	
355 360 365	
ggc acg agc atc aag ggc gag agc gac ttg ccc aag gag aag att ctc	1152
Gly Thr Ser Ile Lys Gly Glu Ser Asp Leu Pro Lys Glu Lys Ile Leu	
370 375 380	

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gaa gat gac ttc agg gtc aag tac tat aac gag tac atc cgt gcc atg      1200
Glu Asp Asp Phe Arg Val Lys Tyr Tyr Asn Glu Tyr Ile Arg Ala Met
385                               390                               395                               400

gtt acc gcc gtg gag ctg gac ggg gtc aac gtc aag ggg tac ttt gcc      1248
Val Thr Ala Val Glu Leu Asp Gly Val Asn Val Lys Gly Tyr Phe Ala
                               405                               410                               415

tgg tcg ctc atg gac aac ttt gag tgg gcg gac ggc tac gtg acg agg      1296
Trp Ser Leu Met Asp Asn Phe Glu Trp Ala Asp Gly Tyr Val Thr Arg
                               420                               425                               430

ttt ggg gtt acg tat gtg gat tat gag aat ggg cag aag cgg ttc ccc      1344
Phe Gly Val Thr Tyr Val Asp Tyr Glu Asn Gly Gln Lys Arg Phe Pro
                               435                               440                               445

aag aag agc gca aag agc ttg aag ccg ctg ttt gac gag ctg att gcg      1392
Lys Lys Ser Ala Lys Ser Leu Lys Pro Leu Phe Asp Glu Leu Ile Ala
                               450                               455                               460

gcg gcg tga
Ala Ala
465

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<210> 90
<211> 466
<212> PRT
<213> Artificial Sequence

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<220>
<223> Synthetic Construct

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<400> 90

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Met Leu Pro Lys Asp Phe Gln Trp Gly Phe Ala Thr Ala Ala Tyr Gln
1                               5                               10                               15

Ile Glu Gly Ala Val Asp Gln Asp Gly Arg Gly Pro Ser Ile Trp Asp
20                               25                               30

Thr Phe Cys Ala Gln Pro Gly Lys Ile Ala Asp Gly Ser Ser Gly Val
35                               40                               45

Thr Ala Cys Asp Ser Tyr Asn Arg Thr Ala Glu Asp Ile Ala Leu Leu
50                               55                               60

Lys Ser Leu Gly Ala Lys Ser Tyr Arg Phe Ser Ile Ser Trp Ser Arg
65                               70                               75                               80

Ile Ile Pro Glu Gly Gly Arg Gly Asp Ala Val Asn Gln Ala Gly Ile
85                               90                               95

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Asp His Tyr Val Lys Phe Val Asp Asp Leu Leu Asp Ala Gly Ile Thr
 100 105 110

Pro Phe Ile Thr Leu Phe His Trp Asp Leu Pro Glu Gly Leu His Gln
 115 120 125

Arg Tyr Gly Gly Leu Leu Asn Arg Thr Glu Phe Pro Leu Asp Phe Glu
 130 135 140

Asn Tyr Ala Arg Val Met Phe Arg Ala Leu Pro Lys Val Arg Asn Trp
 145 150 155 160

Ile Thr Phe Asn Glu Pro Leu Cys Ser Ala Ile Pro Gly Tyr Gly Ser
 165 170 175

Gly Thr Phe Ala Pro Gly Arg Gln Ser Thr Ser Glu Pro Trp Thr Val
 180 185 190

Gly His Asn Ile Leu Val Ala His Gly Arg Ala Val Lys Ala Tyr Arg
 195 200 205

Asp Asp Phe Lys Pro Ala Ser Gly Asp Gly Gln Ile Gly Ile Val Leu
 210 215 220

Asn Gly Asp Phe Thr Tyr Pro Trp Asp Ala Ala Asp Pro Ala Asp Lys
 225 230 235 240

Glu Ala Ala Glu Arg Arg Leu Glu Phe Phe Thr Ala Trp Phe Ala Asp
 245 250 255

Pro Ile Tyr Leu Gly Asp Tyr Pro Ala Ser Met Arg Lys Gln Leu Gly
 260 265 270

Asp Arg Leu Pro Thr Phe Thr Pro Glu Glu Arg Ala Leu Val His Gly
 275 280 285

Ser Asn Asp Phe Tyr Gly Met Asn His Tyr Thr Ser Asn Tyr Ile Arg
 290 295 300

His Arg Ser Ser Pro Ala Ser Ala Asp Asp Thr Val Gly Asn Val Asp
 305 310 315 320

Val Leu Phe Thr Asn Lys Gln Gly Asn Cys Ile Gly Pro Glu Thr Gln
 325 330 335

Ser Pro Trp Leu Arg Pro Cys Ala Ala Gly Phe Arg Asp Phe Leu Val
 340 345 350

Trp Ile Ser Lys Arg Tyr Gly Tyr Pro Pro Ile Tyr Val Thr Glu Asn
 355 360 365

Gly Thr Ser Ile Lys Gly Glu Ser Asp Leu Pro Lys Glu Lys Ile Leu
 370 375 380

Glu Asp Asp Phe Arg Val Lys Tyr Tyr Asn Glu Tyr Ile Arg Ala Met
 385 390 395 400

Val Thr Ala Val Glu Leu Asp Gly Val Asn Val Lys Gly Tyr Phe Ala
 405 410 415

Trp Ser Leu Met Asp Asn Phe Glu Trp Ala Asp Gly Tyr Val Thr Arg
 420 425 430

Phe Gly Val Thr Tyr Val Asp Tyr Glu Asn Gly Gln Lys Arg Phe Pro
 435 440 445

Lys Lys Ser Ala Lys Ser Leu Lys Pro Leu Phe Asp Glu Leu Ile Ala
 450 455 460

Ala Ala
 465

<210> 91
 <211> 2103
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Trichoderma reesei β -Glucosidase D

<220>
 <221> CDS
 <222> (1)..(2103)
 <223> Trichoderma reesei β -Glucosidase D

<400> 91
 atg att ctc ggc tgt gaa agc aca ggt gtc atc tct gcc gtc aaa cac
 Met Ile Leu Gly Cys Glu Ser Thr Gly Val Ile Ser Ala Val Lys His
 1 5 10 15

48

ttt gtc gcc aac gac cag gag cac gag cgg cga gcg gtc gac tgt ctc	96
Phe Val Ala Asn Asp Gln Glu His Glu Arg Arg Ala Val Asp Cys Leu	
20 25 30	
atc acc cag cgg gct ctc cgg gag gtc tat ctg cga ccc ttc cag atc	144
Ile Thr Gln Arg Ala Leu Arg Glu Val Tyr Leu Arg Pro Phe Gln Ile	
35 40 45	
gta gcc cga gat gca agg ccc ggc gca ttg atg aca tcc tac aac aag	192
Val Ala Arg Asp Ala Arg Pro Gly Ala Leu Met Thr Ser Tyr Asn Lys	
50 55 60	
gtc aat ggc aag cac gtc gct gac agc gcc gag ttc ctt cag ggc att	240
Val Asn Gly Lys His Val Ala Asp Ser Ala Glu Phe Leu Gln Gly Ile	
65 70 75 80	
ctc cgg act gag tgg aat tgg gac cct ctc att gtc agc gac tgg tac	288
Leu Arg Thr Glu Trp Asn Trp Asp Pro Leu Ile Val Ser Asp Trp Tyr	
85 90 95	
ggc acc tac acc act att gat gcc atc aaa gcc ggc ctt gat ctc gag	336
Gly Thr Tyr Thr Thr Ile Asp Ala Ile Lys Ala Gly Leu Asp Leu Glu	
100 105 110	
atg ccg ggc gtt tca cga tat cgc ggc aaa tac atc gag tct gct ctg	384
Met Pro Gly Val Ser Arg Tyr Arg Gly Lys Tyr Ile Glu Ser Ala Leu	
115 120 125	
cag gcc cgt ttg ctg aag cag tcc act atc gat gag cgc gct cgc cgc	432
Gln Ala Arg Leu Leu Lys Gln Ser Thr Ile Asp Glu Arg Ala Arg Arg	
130 135 140	
gtg ctc agg ttc gcc cag aag gcc agc cat ctc aag gtc tcc gag gta	480
Val Leu Arg Phe Ala Gln Lys Ala Ser His Leu Lys Val Ser Glu Val	
145 150 155 160	
gag caa ggc cgt gac ttc cca gag gat cgc gtc ctc aac cgt cag atc	528
Glu Gln Gly Arg Asp Phe Pro Glu Asp Arg Val Leu Asn Arg Gln Ile	
165 170 175	
tgc ggc agc agc att gtc cta ctg aag aat gag aac tcc atc tta cct	576
Cys Gly Ser Ser Ile Val Leu Leu Lys Asn Glu Asn Ser Ile Leu Pro	
180 185 190	
ctc ccc aag tcc gtc aag aag gtc gcc ctt gtt ggt tcc cac gtg cgt	624
Leu Pro Lys Ser Val Lys Lys Val Ala Leu Val Gly Ser His Val Arg	
195 200 205	
cta ccg gct atc tcg gga gga ggc agc gcc tct ctt gtc cct tac tat	672
Leu Pro Ala Ile Ser Gly Gly Gly Ser Ala Ser Leu Val Pro Tyr Tyr	
210 215 220	
gcc ata tct cta tac gat gcc gtc tct gag gta cta gcc ggt gcc acg	720
Ala Ile Ser Leu Tyr Asp Ala Val Ser Glu Val Leu Ala Gly Ala Thr	
225 230 235 240	
atc acg cac gag gtc ggt gcc tat gcc cac caa atg ctg ccc gtc atc	768

Ile	Thr	His	Glu	Val	Gly	Ala	Tyr	Ala	His	Gln	Met	Leu	Pro	Val	Ile		
				245					250					255			
gac	gca	atg	atc	agc	aac	gcc	gta	atc	cac	ttc	tac	aac	gac	ccc	atc		816
Asp	Ala	Met	Ile	Ser	Asn	Ala	Val	Ile	His	Phe	Tyr	Asn	Asp	Pro	Ile		
			260					265					270				
gat	gtc	aaa	gac	aga	aag	ctc	ctt	ggc	agt	gag	aac	gta	tcg	tcg	aca		864
Asp	Val	Lys	Asp	Arg	Lys	Leu	Leu	Gly	Ser	Glu	Asn	Val	Ser	Ser	Thr		
		275					280					285					
tcg	ttc	cag	ctc	atg	gat	tac	aac	aac	atc	cca	acg	ctc	aac	aag	gcc		912
Ser	Phe	Gln	Leu	Met	Asp	Tyr	Asn	Asn	Ile	Pro	Thr	Leu	Asn	Lys	Ala		
	290					295					300						
atg	ttc	tgg	ggt	act	ctc	gtg	ggc	gag	ttt	atc	cct	acc	gcc	acg	gga		960
Met	Phe	Trp	Gly	Thr	Leu	Val	Gly	Glu	Phe	Ile	Pro	Thr	Ala	Thr	Gly		
305					310					315					320		
att	tgg	gaa	ttt	ggc	ctc	agt	gtc	ttt	ggc	act	gcc	gac	ctt	tat	att		1008
Ile	Trp	Glu	Phe	Gly	Leu	Ser	Val	Phe	Gly	Thr	Ala	Asp	Leu	Tyr	Ile		
				325					330					335			
gat	aat	gag	ctc	gtg	att	gaa	aat	aca	aca	cat	cag	acg	cgt	gga	acc		1056
Asp	Asn	Glu	Leu	Val	Ile	Glu	Asn	Thr	Thr	His	Gln	Thr	Arg	Gly	Thr		
			340					345					350				
gcc	ttt	ttc	gga	aag	gga	acg	acg	gaa	aaa	gtc	gct	acc	agg	agg	atg		1104
Ala	Phe	Phe	Gly	Lys	Gly	Thr	Thr	Glu	Lys	Val	Ala	Thr	Arg	Arg	Met		
		355					360					365					
gtg	gcc	ggc	agc	acc	tac	aag	ctg	cgt	ctc	gag	ttt	ggg	tct	gcc	aac		1152
Val	Ala	Gly	Ser	Thr	Tyr	Lys	Leu	Arg	Leu	Glu	Phe	Gly	Ser	Ala	Asn		
	370					375					380						
acg	acc	aag	atg	gag	acg	acc	ggt	gtt	gtc	aac	ttt	ggc	ggc	ggt	gcc		1200
Thr	Thr	Lys	Met	Glu	Thr	Thr	Gly	Val	Val	Asn	Phe	Gly	Gly	Gly	Ala		
385					390					395					400		
gta	cac	ctg	ggt	gcc	tgt	ctc	aag	gtc	gac	cca	cag	gag	atg	att	gcg		1248
Val	His	Leu	Gly	Ala	Cys	Leu	Lys	Val	Asp	Pro	Gln	Glu	Met	Ile	Ala		
				405					410					415			
cgg	gcc	gtc	aag	gcc	gca	gcc	gat	gcc	gac	tac	acc	atc	atc	tgc	acg		1296
Arg	Ala	Val	Lys	Ala	Ala	Ala	Asp	Ala	Asp	Tyr	Thr	Ile	Ile	Cys	Thr		
			420					425					430				
gga	ctc	agc	ggc	gag	tgg	gag	tct	gag	ggt	ttt	gac	cgg	cct	cac	atg		1344
Gly	Leu	Ser	Gly	Glu	Trp	Glu	Ser	Glu	Gly	Phe	Asp	Arg	Pro	His	Met		
		435					440					445					
gac	ctg	ccc	cct	ggt	gtg	gac	acc	atg	atc	tcg	caa	gtt	ctt	gac	gcc		1392
Asp	Leu	Pro	Pro	Gly	Val	Asp	Thr	Met	Ile	Ser	Gln	Val	Leu	Asp	Ala		
	450					455					460						
gct	ccc	aat	gct	gta	gtc	gtc	aac	cag	tca	ggc	acc	cca	gtg	aca	atg		1440
Ala	Pro	Asn	Ala	Val	Val	Val	Asn	Gln	Ser	Gly	Thr	Pro	Val	Thr	Met		
465					470					475					480		

agc tgg gct cat aaa gca aag gcc att gtg cag gct tgg tat ggt ggt	1488
Ser Trp Ala His Lys Ala Lys Ala Ile Val Gln Ala Trp Tyr Gly Gly	
485 490 495	
aac gag aca ggc cac gga atc tcc gat gtg ctc ttt ggc aac gtc aac	1536
Asn Glu Thr Gly His Gly Ile Ser Asp Val Leu Phe Gly Asn Val Asn	
500 505 510	
ccg tcg ggg aaa ctc tcc cta tcg tgg cca gtc gat gtg aag cac aac	1584
Pro Ser Gly Lys Leu Ser Leu Ser Trp Pro Val Asp Val Lys His Asn	
515 520 525	
cca gca tat ctc aac tac gcc agc gtt ggt gga cgg gtc ttg tat ggc	1632
Pro Ala Tyr Leu Asn Tyr Ala Ser Val Gly Gly Arg Val Leu Tyr Gly	
530 535 540	
gag gat gtt tac gtt ggc tac aag ttc tac gac aaa acg gag agg gag	1680
Glu Asp Val Tyr Val Gly Tyr Lys Phe Tyr Asp Lys Thr Glu Arg Glu	
545 550 555 560	
gtt ctg ttt cct ttt ggg cat ggc ctg tct tac gct acc ttc aag ctc	1728
Val Leu Phe Pro Phe Gly His Gly Leu Ser Tyr Ala Thr Phe Lys Leu	
565 570 575	
cca gat tct acc gtg agg acg gtc ccc gaa acc ttc cac ccg gac cag	1776
Pro Asp Ser Thr Val Arg Thr Val Pro Glu Thr Phe His Pro Asp Gln	
580 585 590	
ccc aca gta gcc att gtc aag atc aag aac acg agc agt gtc ccg ggc	1824
Pro Thr Val Ala Ile Val Lys Ile Lys Asn Thr Ser Ser Val Pro Gly	
595 600 605	
gcc cag gtc ctg cag tta tac att tcg gcc cca aac tcg cct aca cat	1872
Ala Gln Val Leu Gln Leu Tyr Ile Ser Ala Pro Asn Ser Pro Thr His	
610 615 620	
cgc ccg gtc aag gag ctg cac gga ttc gaa aag gtg tat ctt gaa gct	1920
Arg Pro Val Lys Glu Leu His Gly Phe Glu Lys Val Tyr Leu Glu Ala	
625 630 635 640	
ggc gag gag aag gag gta caa ata ccc att gac cag tac gct act agc	1968
Gly Glu Glu Lys Glu Val Gln Ile Pro Ile Asp Gln Tyr Ala Thr Ser	
645 650 655	
ttc tcg gac gag att gag agc atg tgg aag agc gag agg ggc att tat	2016
Phe Trp Asp Glu Ile Glu Ser Met Trp Lys Ser Glu Arg Gly Ile Tyr	
660 665 670	
gat gtg ctt gta gga ttc tcg agt cag gaa atc tcg ggc aag ggg aag	2064
Asp Val Leu Val Gly Phe Ser Ser Gln Glu Ile Ser Gly Lys Gly Lys	
675 680 685	
ctg att gtg cct gaa acg cga ttc tgg atg ggg ctg tag	2103
Leu Ile Val Pro Glu Thr Arg Phe Trp Met Gly Leu	
690 695 700	

<210> 92
 <211> 700
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 92

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Phe Val Ala Asn Asp Gln Glu His Glu Arg Arg Ala Val Asp Cys Leu
 20 25 30

Ile Thr Gln Arg Ala Leu Arg Glu Val Tyr Leu Arg Pro Phe Gln Ile
 35 40 45

Val Ala Arg Asp Ala Arg Pro Gly Ala Leu Met Thr Ser Tyr Asn Lys
 50 55 60

Val Asn Gly Lys His Val Ala Asp Ser Ala Glu Phe Leu Gln Gly Ile
 65 70 75 80

Leu Arg Thr Glu Trp Asn Trp Asp Pro Leu Ile Val Ser Asp Trp Tyr
 85 90 95

Gly Thr Tyr Thr Thr Ile Asp Ala Ile Lys Ala Gly Leu Asp Leu Glu
 100 105 110

Met Pro Gly Val Ser Arg Tyr Arg Gly Lys Tyr Ile Glu Ser Ala Leu
 115 120 125

Gln Ala Arg Leu Leu Lys Gln Ser Thr Ile Asp Glu Arg Ala Arg Arg
 130 135 140

Val Leu Arg Phe Ala Gln Lys Ala Ser His Leu Lys Val Ser Glu Val
 145 150 155 160

Glu Gln Gly Arg Asp Phe Pro Glu Asp Arg Val Leu Asn Arg Gln Ile
 165 170 175

Cys Gly Ser Ser Ile Val Leu Leu Lys Asn Glu Asn Ser Ile Leu Pro
 180 185 190

Leu Pro Lys Ser Val Lys Lys Val Ala Leu Val Gly Ser His Val Arg
 195 200 205

Leu Pro Ala Ile Ser Gly Gly Gly Ser Ala Ser Leu Val Pro Tyr Tyr
 210 215 220

Ala Ile Ser Leu Tyr Asp Ala Val Ser Glu Val Leu Ala Gly Ala Thr
 225 230 235 240

Ile Thr His Glu Val Gly Ala Tyr Ala His Gln Met Leu Pro Val Ile
 245 250 255

Asp Ala Met Ile Ser Asn Ala Val Ile His Phe Tyr Asn Asp Pro Ile
 260 265 270

Asp Val Lys Asp Arg Lys Leu Leu Gly Ser Glu Asn Val Ser Ser Thr
 275 280 285

Ser Phe Gln Leu Met Asp Tyr Asn Asn Ile Pro Thr Leu Asn Lys Ala
 290 295 300

Met Phe Trp Gly Thr Leu Val Gly Glu Phe Ile Pro Thr Ala Thr Gly
 305 310 315 320

Ile Trp Glu Phe Gly Leu Ser Val Phe Gly Thr Ala Asp Leu Tyr Ile
 325 330 335

Asp Asn Glu Leu Val Ile Glu Asn Thr Thr His Gln Thr Arg Gly Thr
 340 345 350

Ala Phe Phe Gly Lys Gly Thr Thr Glu Lys Val Ala Thr Arg Arg Met
 355 360 365

Val Ala Gly Ser Thr Tyr Lys Leu Arg Leu Glu Phe Gly Ser Ala Asn
 370 375 380

Thr Thr Lys Met Glu Thr Thr Gly Val Val Asn Phe Gly Gly Gly Ala
 385 390 395 400

Val His Leu Gly Ala Cys Leu Lys Val Asp Pro Gln Glu Met Ile Ala
 405 410 415

Arg Ala Val Lys Ala Ala Ala Asp Ala Asp Tyr Thr Ile Ile Cys Thr
 420 425 430

Gly Leu Ser Gly Glu Trp Glu Ser Glu Gly Phe Asp Arg Pro His Met
 435 440 445

Asp Leu Pro Pro Gly Val Asp Thr Met Ile Ser Gln Val Leu Asp Ala
 450 455 460

Ala Pro Asn Ala Val Val Val Asn Gln Ser Gly Thr Pro Val Thr Met
 465 470 475 480

Ser Trp Ala His Lys Ala Lys Ala Ile Val Gln Ala Trp Tyr Gly Gly
 485 490 495

Asn Glu Thr Gly His Gly Ile Ser Asp Val Leu Phe Gly Asn Val Asn
 500 505 510

Pro Ser Gly Lys Leu Ser Leu Ser Trp Pro Val Asp Val Lys His Asn
 515 520 525

Pro Ala Tyr Leu Asn Tyr Ala Ser Val Gly Gly Arg Val Leu Tyr Gly
 530 535 540

Glu Asp Val Tyr Val Gly Tyr Lys Phe Tyr Asp Lys Thr Glu Arg Glu
 545 550 555 560

Val Leu Phe Pro Phe Gly His Gly Leu Ser Tyr Ala Thr Phe Lys Leu
 565 570 575

Pro Asp Ser Thr Val Arg Thr Val Pro Glu Thr Phe His Pro Asp Gln
 580 585 590

Pro Thr Val Ala Ile Val Lys Ile Lys Asn Thr Ser Ser Val Pro Gly
 595 600 605

Ala Gln Val Leu Gln Leu Tyr Ile Ser Ala Pro Asn Ser Pro Thr His
 610 615 620

Arg Pro Val Lys Glu Leu His Gly Phe Glu Lys Val Tyr Leu Glu Ala
 625 630 635 640

Gly Glu Glu Lys Glu Val Gln Ile Pro Ile Asp Gln Tyr Ala Thr Ser
 645 650 655

Phe Trp Asp Glu Ile Glu Ser Met Trp Lys Ser Glu Arg Gly-Ile Tyr
 660 665 670

Asp Val Leu Val Gly Phe Ser Ser Gln Glu Ile Ser Gly Lys Gly Lys
 675 680 685

Leu Ile Val Pro Glu Thr Arg Phe Trp Met Gly Leu
 690 695 700

<210> 93
 <211> 1496
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Maize optimized CBHI

<400> 93
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 cctccggcgc caccctgcacc cagcagaccg gctccgtggt gatcgacgcc aactggcgct 120
 ggacccacgc caccaaactcc tccaccaact gctacgacgg caacacctgg tcctccaccc 180
 tctgcccgga caacgagacc tgcgccaaga actgctgcct cgacggcgcc gcctacgcct 240
 ccacctacgg cgtgaccacc tccggcaact cctctccat cggcttcgtg acccagtcgg 300
 cccagaagaa cgtgggcgc cgcctctacc tcatggcctc cgacaccacc taccaggagt 360
 tcacctcct cggcaacgag ttctccttcg acgtggacgt gtcccagctc ccgtgcggcc 420
 tcaacggcgc cctctacttc gtgtccatgg acgcgacgg cggcgtgtcc aagtaccgga 480
 ccaacaccgc cggcgccaag tacggcaccg gctactgcga ctcccagtc ccgcgcgacc 540
 tcaagtccat caacggccag gccaacgtgg agggctggga gccgtcctcc aacaacgcca 600
 acaccggcat cggcggccac ggctcctgct gctccgagat ggacatctgg gaggccaact 660
 ccatctccga ggccctcacc ccgcaccgt gcaccaccgt gggccaggag atctgcgagg 720
 gcgacggctg cggcggcacc tactccgaca accgctacgg cggcacctgc gaccgggacg 780
 gctgcgactg gaacccttac cgcctcggca acacctcct ctacggcccg ggctcctcct 840
 tcacctcga caccaccaag aagctcaccg tggtgaccca gtccgagacc tccggcgcca 900
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 cctactccgg caacgagctc aacgacgact actgcaccgc cgaggaggcc gagttcggcg 1020
 gctcctcctt ctccgacaag ggcggcctca ccagttcaa gaaggccacc tccggcgcca 1080
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cctacccgac caacgagacc tctccacccc cgggcgccgt ggcgggctcc tgctccacct 1200
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 gcaaccgcgc gggcaccacc accaccgcgc gcccgccac caccaccggc tcttccccgg 1380
 gcccgaacca gtcccactac ggccagtgcg gcggcatcgg ctactccggc ccgaccgtgt 1440
 gcgcctccgg caccacctgc cagggtgctca acccgtaacta ctcccagtgc ctctag 1496

<210> 94
 <211> 1365
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Maize optimized CBHII

<400> 94
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 aactggtccg gcccgacctg ctgcgcctcc ggctccacct gcgtgtactc caacgactac 120
 tactcccagt gcctcccggg cgcgcctcc tctcctcct ccaccgcgc cgcctccacc 180
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 atgtggctcg acaccctcga caagaccccg ctcatggagc agaccctcgc cgacatccgc 480
 accgccaaca agaacggcgg caactacgcc ggccagttcg tgggtgtacga cctcccgga 540
 cgcgactgcg ccgccctcgc ctccaacggc gactactcca tcgcgcacgg cggcgtggcc 600
 aagtacaaga actacatcga caccatccgc cagatcgtgg tggagtactc cgacatccgc 660
 acctcctcgc tgatcgagcc ggactccctc gccaacctcg tgaccaacct cggcaccgcc 720
 aagtgcgcca acgcccagtc cgcctacctc gactgcatca actaogcgt gaccagctc 780
 aacctccga acgtggccat gtacctcgac gccggccaag ccggctgggt cggctggccg 840
 gccaaaccagg acccggcgc ccagctcttc gccaacgtgt acaagaacgc ctctccccg 900
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 ccgcgctcct acaccaggg caacgcctg tacaacgaga agctctacat ccacgccatc 1020
 ggcccgcctc tcgccaacca cggctggctc aacgccttct tcatcaccga ccagggccgc 1080

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gtgaagccgg gcggcgagtg cgacggcaac tccgactcct ccgccccgcg cttcgactcc 1260
cactgcgccc tcccggacgc cctccagccg gccccgcagg ccggcgccctg gttccaggcc 1320
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<210> 95
<211> 1317
<212> DNA
<213> Artificial Sequence

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<220>
<223> Maize optimized EGLI

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<400> 95
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tggatgcacg acgccaacta caactcctgc accgtgaacg gcggcggtga caccaccctc 180
tgcccggacg agggcacctg cggcaagaac tgcttcatcg agggcggtga ctacgcgcgc 240
tccggcggtga ccacctccgg ctctcctcct accatgaacc agtacatgcc gtcctcctcc 300
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aacaccgcg gcgccaacta cggctccggc tactgcgacg ccagtgccc ggtgcagacc 540
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tccaacatcc gctggggcga catcggtctc accaccaact ccaccgccc gccgcccgcg 1140

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ccggcctcct ccaccacctt ctccaccacc cgccgctcct ccaccacctc ctctctccccg 1200
 tcctgcaccc agaccactg gggccagtgc ggccggcatcg gctactccgg ctgcaagacc 1260
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<210> 96
 <211> 1401
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Maize optimized BGLII

<400> 96
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 gtggaccagg acggccgcgg cccgtccatc tgggacacct tctgcgcca gccgggcaag 120
 atcgccgacg gctcctccgg cgtgaccgcc tgcgactcct acaaccgcac cgccgaggac 180
 atcgccctcc tcaagtcctt cggcgccaag tctaccgct tctccatctc ctgggtccgc 240
 atcatcccgg agggcgggccg cggcgacgcc gtgaaccagg ccggcatcga ccactacgtg 300
 aagttcgtgg acgacctcct cgacgccggc atcaccccg tcatcacctt cttccactgg 360
 gacotcccgg agggcctcca ccagcgctac ggccggcctc tcaaccgcac cgagttcccg 420
 ctcgacttcg agaactacgc ccgctgtgat ttccgcgcc tcccgaaggt gcgcaactgg 480
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 ccgggcccgc agtccacctc cgagccgtgg accgtgggcc acaacatcct cgtggcccac 600
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 ggcatcgtgc tcaacggcga cttcacctac ccgtgggacg ccgccgaccc ggccgacaag 720
 gaggcgcgcg agcgcgcctt cgagttcttc accgcttggg tcgccgaccc gatctacctc 780
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 aactacatcc gccaccgctc ctcccgggcc tccgccgacg acaccgtggg caacgtggac 960
 gtgctcttca ccaacaagca gggcaactgc atcgcccggg agaccagtc cccgtggctc 1020
 cgcccgtgcg ccgccggctt ccgcgacttc ctcggtgtga tctccaagcg ctacggctac 1080
 ccgccgatct acgtgaccga gaacggcacc tccatcaagg gcgagtcga cctcccgaag 1140
 gagaagatcc tcgaggacga cttccgcgtg aagtactaca acgagtacat ccgcgccatg 1200
 gtgaccgcgg tggagctcga cggcgtgaac gtgaaggggt acttcgcctg gtccctcatg 1260

gacaacttcg agtgggcccga cggctacgtg acccgcttcg gcgtgacctg cgtggactac 1320
 gagaacggcc agaagcgctt cccgaagaag tccgccaaagt cctcaagcc gctcttcgac 1380
 gagctcatcg ccgccgccta g 1401

<210> 97
 <211> 2103
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Maize optimized CEL3D

<400> 97
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 gaccaggagc acgagcgccc cgcggtggac tgctcatca cccagcgccc cctccgagag 120
 gtgtacctcc gcccggtcca gatcgtggcc cgcgacgccc gcccgggccc cctcatgacc 180
 tcctacaaca aggtgaacgg caagcacgtg gccgactccg ccgagttcct ccagggcacc 240
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 accatcgagc ccatcaaggc cggcctcgac ctcgagatgc cgggcgtgtc ccgctaccgc 360
 ggcaagtaca tcgagtcggc cctccaggcc cgcctcctca agcagtcacc catcgagag 420
 cgcgcccggc gcgtgctccg ctccgcccag aaggcctccc acctcaaggt gtccgaggtg 480
 gagcaggggc gcgacttccc ggaggaccgc gtgctcaacc gccagatctg cggctcctcc 540
 atcgtgctcc tcaagaacga gaactccatc ctcccgctcc cgaagtcggt gaagaaggtg 600
 gccctcggtg gctccacgt gcgcctccc gccatctccg gcggcggtc cgcctccctc 660
 gtgccgtact acgccatctc cctctacgac gccgtgtccg aggtgctcgc cggcgccacc 720
 atcaccacgc aggtgggggc ctacgcccac cagatgctcc cggtgatcga cgccatgac 780
 tccaacgccg tgatccactt ctacaacgac ccgatcgagc tgaaggaccg caagctcctc 840
 ggctccgaga acgtgtcctc cacctccttc cagctcatgg actacaacaa catcccgacc 900
 ctcaacaagg ccatgttctg gggcaccctc gtggggcaggt tcatcccgac cgccaccggc 960
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 gagaaggtgg ccacccgccc catggtggcc ggctccacct acaagctccg cctcgagttc 1140
 ggctccgcca acaccaccaa gatggagacc accggcggtg tgaacttcgg cggcgggccc 1200
 gtgcacctcg gcgcctgcct caaggtggac ccgcaggaga tgatcgccc cgcggtgaag 1260

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gccgccgccg acgccgacta caccatcatc tgcaccggcc tctccggcga gtgggagtc 1320
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cacggcatct ccgacgtgct ctccggcaac gtgaaccctg ccggcaagct ctccctctcc 1560
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gtgcgcaccg tgccggagac ctccaccccg gaccagccga ccgtggccat cgtgaagatc 1800
aagaacacct cctccgtgcc gggcgcccag gtgctccagc tctacatctc cgcgccgaac 1860
tccccgaccc accgcccggg gaaggagctc cagggttcg agaaggtgta cctcgaggcc 1920
ggcgaggaga aggaggtgca gatcccgatc gaccagtaag ccacctcctt ctgggacgag 1980
atcgagtcca tgtggaagtc cgagcgcggc atctacgacg tgctcgtggg cttctcctcc 2040
caggagatct ccggcaaggg caagctcatc gtgcgggaga cccgcttctg gatgggcctc 2100
tag 2103

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<210> 98
 <211> 420
 <212> DNA
 <213> Zea mays

<220>
 <223> Q protein promoter

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<400> 98
gggctggtaa attacttggg agcaatggta tgcaaactct ttgcatgtac gcaaaactag 60
ctagttgtca caagttgtat atcgattcgt cgcgtttcaa caactcatgc aacattacaa 120
acaagtaaca caatattaca aagttagttt catacaaagc aagaaaagga caataatact 180
tgacatgtaa agtgaagctt attatacttc ctaatccaac acaaaacaaa aaaaagttgc 240
acaaagggtcc aaaaatccac atcaaccatt aacctatacg taaagtgagt gatgagtcac 300
attatccaac aaatgtttat caatgtggta tcatacaagc attgacatcc cataaatgca 360
agaaattgtg ccaacaaagc tataagtaac cctcatatgt atttgactc atgcatcaca 420

```

<210> 99
 <211> 1188

<212> DNA
 <213> artificial sequence

<220>
 <223> synthetic ferulic acid esterase

<400> 99
 atggccgcct ccctcccgac catgccgcgcg tccggctacg accaggtgcg caacggcgtg 60
 ccgcgcggcc aggtggtgaa catctcctac ttctccaccg ccaccaactc caccgcgccg 120
 gccgcggtgt acctcccgcc gggctactcc aaggacaaga agtactccgt gctctacctc 180
 ctccacggca tcggcggctc cgagaacgac tggttcgagg gcggcggccg cgccaacgtg 240
 atgcgcgaca acctcatcgc cgagggcaag atcaagccgc tcatcatcgt gaccccgaaac 300
 accaacgcgcg ccggcccggg catcgccgac ggctacgaga acttcaccaa ggacctctc 360
 aactccctca tcccgtaacat cgagtcacaac tactccgtgt acaccgaccg cgagcaccgc 420
 gccatcgccg gcctctctat gggcggcggc cagtccttca acatcggcct caccaacctc 480
 gacaagtctg cctacatcgg ccgatctcc gccgccccga acacctacc gaacgagcgc 540
 ctcttcccg acggcggcaa ggccgcccgc gagaagctca agctcctctt catcgctgc 600
 ggcaccaacg actccctcat cggcttcggc cagcgcgtgc acgagtactg cgtggccaac 660
 aacatcaacc acgtgtactg gctcatccag ggccggcgcc acgacttcaa cgtgtggaag 720
 ccgggcctct ggaacttctt ccagatggcc gacgaggccg gcctcaccgc cgacggcaac 780
 accccggtgc cgaccccgct cccgaagccg gccaacaccc gcatcgaggc cgaggactac 840
 gacggcatca actcctctc catcgagatc atcggcgtgc cgcgggaggg cggccgcggc 900
 atcggctaca tcacctccg cgactacctc gtgtacaagt ccatcgactt cggcaacggc 960
 gccacctctt tcaaggccaa ggtggccaac gccaacacct ccaacatcga gcttcgcctc 1020
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 acctacgagg agcagacctg ctccatctcc aaggtgaccg gcatcaacga cctctacctc 1140
 gtgttcaagg gcccggtgaa catcgactgg ttacacttcg gcgtgtag 1188

<210> 100
 <211> 395
 <212> PRT
 <213> artificial sequence

<220>
 <223> synthetic ferulic acid esterase

<400> 100

Met Ala Ala Ser Leu Pro Thr Met Pro Pro Ser Gly Tyr Asp Gln Val
 1 5 10 15
 Arg Asn Gly Val Pro Arg Gly Gln Val Val Asn Ile Ser Tyr Phe Ser
 20 25 30
 Thr Ala Thr Asn Ser Thr Arg Pro Ala Arg Val Tyr Leu Pro Pro Gly
 35 40 45
 Tyr Ser Lys Asp Lys Lys Tyr Ser Val Leu Tyr Leu Leu His Gly Ile
 50 55 60
 Gly Gly Ser Glu Asn Asp Trp Phe Glu Gly Gly Gly Arg Ala Asn Val
 65 70 75 80
 Ile Ala Asp Asn Leu Ile Ala Glu Gly Lys Ile Lys Pro Leu Ile Ile
 85 90 95
 Val Thr Pro Asn Thr Asn Ala Ala Gly Pro Gly Ile Ala Asp Gly Tyr
 100 105 110
 Glu Asn Phe Thr Lys Asp Leu Leu Asn Ser Leu Ile Pro Tyr Ile Glu
 115 120 125
 Ser Asn Tyr Ser Val Tyr Thr Asp Arg Glu His Arg Ala Ile Ala Gly
 130 135 140
 Leu Ser Met Gly Gly Gly Gln Ser Phe Asn Ile Gly Leu Thr Asn Leu
 145 150 155 160
 Asp Lys Phe Ala Tyr Ile Gly Pro Ile Ser Ala Ala Pro Asn Thr Tyr
 165 170 175
 Pro Asn Glu Arg Leu Phe Pro Asp Gly Gly Lys Ala Ala Arg Glu Lys
 180 185 190
 Leu Lys Leu Leu Phe Ile Ala Cys Gly Thr Asn Asp Ser Leu Ile Gly
 195 200 205
 Phe Gly Gln Arg Val His Glu Tyr Cys Val Ala Asn Asn Ile Asn His
 210 215 220
 Val Tyr Trp Leu Ile Gln Gly Gly Gly His Asp Phe Asn Val Trp Lys
 225 230 235 240

Pro Gly Leu Trp Asn Phe Leu Gln Met Ala Asp Glu Ala Gly Leu Thr
 245 250 255

Arg Asp Gly Asn Thr Pro Val Pro Thr Pro Ser Pro Lys Pro Ala Asn
 260 265 270

Thr Arg Ile Glu Ala Glu Asp Tyr Asp Gly Ile Asn Ser Ser Ser Ile
 275 280 285

Glu Ile Ile Gly Val Pro Pro Glu Gly Gly Arg Gly Ile Gly Tyr Ile
 290 295 300

Thr Ser Gly Asp Tyr Leu Val Tyr Lys Ser Ile Asp Phe Gly Asn Gly
 305 310 315 320

Ala Thr Ser Phe Lys Ala Lys Val Ala Asn Ala Asn Thr Ser Asn Ile
 325 330 335

Glu Leu Arg Leu Asn Gly Pro Asn Gly Thr Leu Ile Gly Thr Leu Ser
 340 345 350

Val Lys Ser Thr Gly Asp Trp Asn Thr Tyr Glu Glu Gln Thr Cys Ser
 355 360 365

Ile Ser Lys Val Thr Gly Ile Asn Asp Leu Tyr Leu Val Phe Lys Gly
 370 375 380

Pro Val Asn Ile Asp Trp Phe Thr Phe Gly Val
 385 390 395

<210> 101
 <211> 1188
 <212> DNA
 <213> artificial sequence

<220>
 <223> plasmid 13036

<400> 101
 atggcgcct ccctcccgac catgccgccg tccggctacg accaggtgcg caacggcgtg 60
 ccgcgcggcc aggtggtgaa catctcctac ttctccaccg ccaccaactc caccgcgccg 120
 gcccgcgtgt acctcccgcc gggctactcc aaggacaaga agtactccgt gctctacctc 180
 ctccacggca tcggcggctc cgagaacgac tggttcgagg gcggcgggccg cgccaacgtg 240

atcgccgaca acctcatcgc cgagggcaag atcaagccgc tcatcatcgt gaccccgaaac 300
 accaacgccg ccggcccggg catcgccgac ggctacgaga acttcaccaa ggacctctc 360
 aactccctca tcccgtagat cgaggtccaac tactccgtgt acaccgaccg cgagcaccgc 420
 gccatcgccg gcctctctat gggcgggcggc cagtccttca acatcggcct caccaacctc 480
 gacaagttcg cctacatcgg ccgcatctcc gccgccccga acacctacc gaacgagcgc 540
 ctcttcccg acggcgggcaa ggccgcccgc gagaagctca agctctctt catcgctgc 600
 ggcaccaacg actccctcat cggttcggc cagcgcgtgc acgagtactg cgtggccaac 660
 aacatcaacc acgtgtactg gctcatccag ggcgggggcc acgaattcaa cgtgtggaag 720
 ccgggctct ggaacttct ccagatggcc gacgaggccg gcctcaccg cgacggcaac 780
 accccggtgc cgaccccgtc ccgaagccg gccaacacc gcacgagggc cgaggactac 840
 gacggcatca actctctct catcgagatc atcggcgtgc cgccggaggg cggccgcggc 900
 atcggctaca tcacctcgg cgactacct gtgtacaagt ccatcgactt cggcaacggc 960
 gccacctct tcaaggccaa ggtggccaac gccaacacct ccaacatga gtttcgctc 1020
 aacggcccga acggcacct catcggcacc ctctccgtga agtcaccgg cgactggaac 1080
 acctacgagg agcagacct ctccatctcc aaggtgaccg gcatcaacga cctctacctc 1140
 gtgttcaagg gcccggtgaa catcgactgg ttcaccttcg gcgtgtag 1188

<210> 102
 <211> 395
 <212> PRT
 <213> artificial sequence

<220>
 <223> plasmid 13036
 <400> 102

Met Ala Ala Ser Leu Pro Thr Met Pro Pro Ser Gly Tyr Asp Gln Val
 1 5 10 15

Arg Asn Gly Val Pro Arg Gly Gln Val Val Asn Ile Ser Tyr Phe Ser
 20 25 30

Thr Ala Thr Asn Ser Thr Arg Pro Ala Arg Val Tyr Leu Pro Pro Gly
 35 40 45

Tyr Ser Lys Asp Lys Lys Tyr Ser Val Leu Tyr Leu Leu His Gly Ile
 50 55 60

Gly Gly Ser Glu Asn Asp Trp Phe Glu Gly Gly Gly Arg Ala Asn Val
 65 70 75 80
 Ile Ala Asp Asn Leu Ile Ala Glu Gly Lys Ile Lys Pro Leu Ile Ile
 85 90 95
 Val Thr Pro Asn Thr Asn Ala Ala Gly Pro Gly Ile Ala Asp Gly Tyr
 100 105 110
 Glu Asn Phe Thr Lys Asp Leu Leu Asn Ser Leu Ile Pro Tyr Ile Glu
 115 120 125
 Ser Asn Tyr Ser Val Tyr Thr Asp Arg Glu His Arg Ala Ile Ala Gly
 130 135 140
 Leu Ser Met Gly Gly Gly Gln Ser Phe Asn Ile Gly Leu Thr Asn Leu
 145 150 155 160
 Asp Lys Phe Ala Tyr Ile Gly Pro Ile Ser Ala Ala Pro Asn Thr Tyr
 165 170 175
 Pro Asn Glu Arg Leu Phe Pro Asp Gly Gly Lys Ala Ala Arg Glu Lys
 180 185 190
 Leu Lys Leu Leu Phe Ile Ala Cys Gly Thr Asn Asp Ser Leu Ile Gly
 195 200 205
 Phe Gly Gln Arg Val His Glu Tyr Cys Val Ala Asn Asn Ile Asn His
 210 215 220
 Val Tyr Trp Leu Ile Gln Gly Gly Gly His Asp Phe Asn Val Trp Lys
 225 230 235 240
 Pro Gly Leu Trp Asn Phe Leu Gln Met Ala Asp Glu Ala Gly Leu Thr
 245 250 255
 Arg Asp Gly Asn Thr Pro Val Pro Thr Pro Ser Pro Lys Pro Ala Asn
 260 265 270
 Thr Arg Ile Glu Ala Glu Asp Tyr Asp Gly Ile Asn Ser Ser Ser Ile
 275 280 285

Glu Ile Ile Gly Val Pro Pro Glu Gly Gly Arg Gly Ile Gly Tyr Ile
 290 295 300
 Thr Ser Gly Asp Tyr Leu Val Tyr Lys Ser Ile Asp Phe Gly Asn Gly
 305 310 315 320
 Ala Thr Ser Phe Lys Ala Lys Val Ala Asn Ala Asn Thr Ser Asn Ile
 325 330 335
 Glu Leu Arg Leu Asn Gly Pro Asn Gly Thr Leu Ile Gly Thr Leu Ser
 340 345 350
 Val Lys Ser Thr Gly Asp Trp Asn Thr Tyr Glu Glu Gln Thr Cys Ser
 355 360 365
 Ile Ser Lys Val Thr Gly Ile Asn Asp Leu Tyr Leu Val Phe Lys Gly
 370 375 380
 Pro Val Asn Ile Asp Trp Phe Thr Phe Gly Val
 385 390 395

<210> 103
 <211> 1245
 <212> DNA
 <213> artificial sequence

<220>
 <223> plasmid 13038

<400> 103
 atgaggggtgt tgctcggttgc cctcgctctc ctggctctcg ctgcgagcgc cacctccatg 60
 gccgcctccc tcccgaccat gccgcggtcc ggctacgacc aggtgcgcaa cggcgtgccg 120
 cgcggccagg tggatgaacat ctctacttc tccaccgcca ccaactccac ccgcccggcc 180
 cgcgtgtacc tcccgccggg ctactccaag gacaagaagt actccgtgct ctacctctc 240
 cacggcatcg gcggctccga gaacgactgg ttcgagggcg gcggccgcgc caacgtgatc 300
 gccgacaacc tcatcgccga gggcaagatc aagccgctca tcatcgtgac cccgaacacc 360
 aacgcgcgcg gcccgggcat cgcgcgacggc tacgagaact tcaccaagga cctcctcaac 420
 tccctcatcc cgtacatcga gtccaactac tccgtgtaca ccgaccgcga gcaccgcgcc 480
 atcgccggcc tctctatggg cggcgggccag tccctcaaca tcggcctcac caacctcgac 540
 aagttcgctt acatcgggcc gatctccgcc gccccgaaca cctacccgaa cgagcgcttc 600
 ttcccggaag gcggcaaggc cgcgcgcgag aagctcaagc tcctcttcat cgctcgcgcc 660


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accaacgact cctcatcgg cttcggccag cgcgtgcacg agtactgcgt ggccaacaac      720
atcaaccacg tgtactggct catccagggc ggcggccacg acttcaacgt gtggaagccg      780
ggcctctgga acttcctcca gatggccgac gaggccggcc tcacccgcga cggcaacacc      840
ccggtgccga ccccgcccc gaagccggcc aacaccgcga tcgaggccga ggactacgac      900
ggcatcaact cctcctccat cgagatcadc ggcgtgccgc cggagggcgg ccgcggcatc     960
ggctacatca cctcggcgga ctacctcgtg tacaagtcca tcgacttcgg caacggcgcc     1020
acctccttca aggccaaagg ggccaacgcc aacacctcca acatcgagct tcgcctcaac     1080
ggcccgaacg gcacctcat cggcacccctc tccgtgaagt ccaccggcga ctggaacacc     1140
tacgaggagc agacctgctc catctccaag gtgaccggca tcaacgacct ctacctcgtg     1200
ttcaagggcc cggatgaacat cgactggttc accttcggcg tgtag                      1245

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<210> 104
 <211> 414
 <212> PRT
 <213> artificial sequence

<220>
 <223> plasmid 13038 aa

<400> 104

```

Met Arg Val Leu Leu Val Ala Leu Ala Leu Leu Ala Leu Ala Ala Ser
1           5           10           15

```

```

Ala Thr Ser Met Ala Ala Ser Leu Pro Thr Met Pro Pro Ser Gly Tyr
20           25           30

```

```

Asp Gln Val Arg Asn Gly Val Pro Arg Gly Gln Val Val Asn Ile Ser
35           40           45

```

```

Tyr Phe Ser Thr Ala Thr Asn Ser Thr Arg Pro Ala Arg Val Tyr Leu
50           55           60

```

```

Pro Pro Gly Tyr Ser Lys Asp Lys Lys Tyr Ser Val Leu Tyr Leu Leu
65           70           75           80

```

```

His Gly Ile Gly Gly Ser Glu Asn Asp Trp Phe Glu Gly Gly Gly Arg
85           90           95

```

```

Ala Asn Val Ile Ala Asp Asn Leu Ile Ala Glu Gly Lys Ile Lys Pro
100          105          110

```

Leu Ile Ile Val Thr Pro Asn Thr Asn Ala Ala Gly Pro Gly Ile Ala
 115 120 125

Asp Gly Tyr Glu Asn Phe Thr Lys Asp Leu Leu Asn Ser Leu Ile Pro
 130 135 140

Tyr Ile Glu Ser Asn Tyr Ser Val Tyr Thr Asp Arg Glu His Arg Ala
 145 150 155 160

Ile Ala Gly Leu Ser Met Gly Gly Gly Gln Ser Phe Asn Ile Gly Leu
 165 170 175

Thr Asn Leu Asp Lys Phe Ala Tyr Ile Gly Pro Ile Ser Ala Ala Pro
 180 185 190

Asn Thr Tyr Pro Asn Glu Arg Leu Phe Pro Asp Gly Gly Lys Ala Ala
 195 200 205

Arg Glu Lys Leu Lys Leu Leu Phe Ile Ala Cys Gly Thr Asn Asp Ser
 210 215 220

Leu Ile Gly Phe Gly Gln Arg Val His Glu Tyr Cys Val Ala Asn Asn
 225 230 235 240

Ile Asn His Val Tyr Trp Leu Ile Gln Gly Gly Gly His Asp Phe Asn
 245 250 255

Val Trp Lys Pro Gly Leu Trp Asn Phe Leu Gln Met Ala Asp Glu Ala
 260 265 270

Gly Leu Thr Arg Asp Gly Asn Thr Pro Val Pro Thr Pro Ser Pro Lys
 275 280 285

Pro Ala Asn Thr Arg Ile Glu Ala Glu Asp Tyr Asp Gly Ile Asn Ser
 290 295 300

Ser Ser Ile Glu Ile Ile Gly Val Pro Pro Glu Gly Gly Arg Gly Ile
 305 310 315 320

Gly Tyr Ile Thr Ser Gly Asp Tyr Leu Val Tyr Lys Ser Ile Asp Phe
 325 330 335

Gly Asn Gly Ala Thr Ser Phe Lys Ala Lys Val Ala Asn Ala Asn Thr
 340 345 350

Ser Asn Ile Glu Leu Arg Leu Asn Gly Pro Asn Gly Thr Leu Ile Gly
 355 360 365

Thr Leu Ser Val Lys Ser Thr Gly Asp Trp Asn Thr Tyr Glu Glu Gln
 370 375 380

Thr Cys Ser Ile Ser Lys Val Thr Gly Ile Asn Asp Leu Tyr Leu Val
 385 390 395 400

Phe Lys Gly Pro Val Asn Ile Asp Trp Phe Thr Phe Gly Val
 405 410

<210> 105
 <211> 1425
 <212> DNA
 <213> artificial sequence

<220>
 <223> plasmid 13039

<400> 105
 atgctggcgg ctctggccac gtcgcagctc gtcgcaacgc gcgccggcct gggcgccccg 60
 gacgcgtcca cggtccgccc cggcgcgcgc cagggcctga gggggggccc ggcgtcgggc 120
 gcggcggaaca cgctcagcat gcggaccagc gcgcgcgcgc cggccaggca ccagcaccag 180
 caggcgcgcc gcggggccag gttcccgctc ctgcgtgtgt gcgccagcgc cggcgccatg 240
 gccgcctccc tcccgaccat gccgcgcgtc ggctacgacc aggtgcgcaa cggcggtgcc 300
 cgcggccagg tgggtgaacat ctctacttcc tccaccgcca ccaactccac ccgcccggcc 360
 cgcgtgtacc tcccgccggg ctactccaag gacaagaagt actccgtgct ctacctctc 420
 cacggcatcg gcggctccga gaacgactgg ttgcagggcg gcggccgcgc caacgtgatc 480
 gccgacaacc tcctcgccga gggcaagatc aagccgctca tcctcgtgac ccggaacacc 540
 aacgccgcgc gcccgggcat cgcgcgagcgc tacgagaact tcaccaagga cctcctcaac 600
 tccctcatcc cgtacatcga gtccaactac tccgtgtaca ccgaccgcga gcaccgcgcc 660
 atcgccggcc tctctatggg cggcgggccag tccctcaaca tcggcctcac caacctcgac 720
 aagttcgctt acatcgggcc gatctccgcc gcccgaaca cctaccgaa cgagcgctc 780
 ttcccggaag gcggcaaggc cggccgcgag aagctcaagc tctcttcat cgctcgcgcc 840
 accaaccgact cctcatcggt cttcgggccag cgcgtgcacg agtactgcgt ggccaacaac 900

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atcaaccacg tgtactggct catccagggc ggcgggccacg acttcaacgt gtggaagccg      960
ggcctctgga acttcctcca gatggccgac gaggccggcc tcaccgcga cggcaacacc      1020
ccggtgccga ccccgcccc gaagccggcc aacaccgcga tcgaggccga ggactacgac      1080
ggcatcaact cctcctccat cgagatcatc ggcggtgccgc cggagggcgg ccgcggcatc      1140
ggctacatca cctccggcga ctacctcgtg tacaagtcca tcgacttcgg caacggcgcc      1200
acctccttca aggccaaggt ggccaacgcc aacacctcca acatcgagct tcgcctcaac      1260
ggcccgaacg gcacctcat cggcacctc tccgtgaagt ccaccggcga ctggaacacc      1320
tacgaggagc agacctgctc catctccaag gtgaccggca tcaacgacct ctacctcgtg      1380
ttcaagggcc cggtgaacat cgactggttc accttcggcg tgtag                        1425

```

```

<210> 106
<211> 474
<212> PRT
<213> artificial sequence

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```

<220>
<223> plasmid 13039 aa

```

```

<400> 106

```

```

Met Leu Ala Ala Leu Ala Thr Ser Gln Leu Val Ala Thr Arg Ala Gly
1           5           10          15

```

```

Leu Gly Val Pro Asp Ala Ser Thr Phe Arg Arg Gly Ala Ala Gln Gly
      20           25           30

```

```

Leu Arg Gly Ala Arg Ala Ser Ala Ala Ala Asp Thr Leu Ser Met Arg
      35           40           45

```

```

Thr Ser Ala Arg Ala Ala Pro Arg His Gln His Gln Gln Ala Arg Arg
      50           55           60

```

```

Gly Ala Arg Phe Pro Ser Leu Val Val Cys Ala Ser Ala Gly Ala Met
65           70           75           80

```

```

Ala Ala Ser Leu Pro Thr Met Pro Pro Ser Gly Tyr Asp Gln Val Arg
      85           90           95

```

```

Asn Gly Val Pro Arg Gly Gln Val Val Asn Ile Ser Tyr Phe Ser Thr
      100          105          110

```

Ala Thr Asn Ser Thr Arg Pro Ala Arg Val Tyr Leu Pro Pro-Gly Tyr
 115 120 125

Ser Lys Asp Lys Lys Tyr Ser Val Leu Tyr Leu Leu His Gly Ile Gly
 130 135 140

Gly Ser Glu Asn Asp Trp Phe Glu Gly Gly Gly Arg Ala Asn Val Ile
 145 150 155 160

Ala Asp Asn Leu Ile Ala Glu Gly Lys Ile Lys Pro Leu Ile Ile Val
 165 170 175

Thr Pro Asn Thr Asn Ala Ala Gly Pro Gly Ile Ala Asp Gly Tyr Glu
 180 185 190

Asn Phe Thr Lys Asp Leu Leu Asn Ser Leu Ile Pro Tyr Ile Glu Ser
 195 200 205

Asn Tyr Ser Val Tyr Thr Asp Arg Glu His Arg Ala Ile Ala Gly Leu
 210 215 220

Ser Met Gly Gly Gly Gln Ser Phe Asn Ile Gly Leu Thr Asn Leu Asp
 225 230 235 240

Lys Phe Ala Tyr Ile Gly Pro Ile Ser Ala Ala Pro Asn Thr Tyr Pro
 245 250 255

Asn Glu Arg Leu Phe Pro Asp Gly Gly Lys Ala Ala Arg Glu Lys Leu
 260 265 270

Lys Leu Leu Phe Ile Ala Cys Gly Thr Asn Asp Ser Leu Ile Gly Phe
 275 280 285

Gly Gln Arg Val His Glu Tyr Cys Val Ala Asn Asn Ile Asn His Val
 290 295 300

Tyr Trp Leu Ile Gln Gly Gly Gly His Asp Phe Asn Val Trp Lys Pro
 305 310 315 320

Gly Leu Trp Asn Phe Leu Gln Met Ala Asp Glu Ala Gly Leu Thr Arg
 325 330 335

Asp Gly Asn Thr Pro Val Pro Thr Pro Ser Pro Lys Pro Ala Asn Thr
 340 345 350

Arg Ile Glu Ala Glu Asp Tyr Asp Gly Ile Asn Ser Ser Ser Ile Glu
 355 360 365
 Ile Ile Gly Val Pro Pro Glu Gly Gly Arg Gly Ile Gly Tyr Ile Thr
 370 375 380
 Ser Gly Asp Tyr Leu Val Tyr Lys Ser Ile Asp Phe Gly Asn Gly Ala
 385 390 395 400
 Thr Ser Phe Lys Ala Lys Val Ala Asn Ala Asn Thr Ser Asn Ile Glu
 405 410 415
 Leu Arg Leu Asn Gly Pro Asn Gly Thr Leu Ile Gly Thr Leu Ser Val
 420 425 430
 Lys Ser Thr Gly Asp Trp Asn Thr Tyr Glu Glu Gln Thr Cys Ser Ile
 435 440 445
 Ser Lys Val Thr Gly Ile Asn Asp Leu Tyr Leu Val Phe Lys Gly Pro
 450 455 460
 Val Asn Ile Asp Trp Phe Thr Phe Gly Val
 465 470

<210> 107
 <211> 1263
 <212> DNA
 <213> artificial sequence

<220>
 <223> plasmid 13347

<400> 107
 atgaggggtgt tgctcgttgc cctcgctctc ctggctctcg ctgcgagcgc cacctccatg 60
 gccgcctccc tcccgaccat gccgccgtcc ggctacgacc aggtgcgcaa cggcgtgccg 120
 cgcggccagg tggtgaacat ctctacttc tccaccgcca ccaactccac ccgcccggcc 180
 cgcgtgtacc tcccgccggg ctactccaag gacaagaagt actccgtgct ctacctctc 240
 cacggcatcg gcggctccga gaacgactgg ttcgagggcg gcggccgcgc caacgtgatc 300
 gccgacaacc tcatcgccga gggcaagatc aagccgctca tcatcgtgac cccgaacacc 360
 aacgccgccg gcccgggcat cgccgacggc tacgagaact tcaccaagga cctcctcaac 420
 tccctcatcc cgtacatcga gtccaactac tccgtgtaca ccgaccgcga gcaccgcgcc 480

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atcgccggcc tctctatggg cggcggccag tccttcaaca tcggcctcac caacctcgac    540
aagttcgcct acatcggccc gatctccgcc gcccgaaca cctaccgaa cgagcgctc    600
ttcccggacg gcggcaaggc cggccgcgag aagctcaagc tcctttcat cgctgcggc    660
accaacgact cctcatcgg cttcggccag cgcgtgcacg agtactgctt ggccaacaac    720
atcaaccacg tgtactggct catccagggc ggcggccacg acttcaacgt gtggaagccg    780
ggcctctgga acttcctcca gatggccgac gaggccggcc tcaccgcga cggcaacacc    840
ccggtgccga ccccgctccc gaagccggcc aacaccgca tcgaggccga ggactacgac    900
ggcatcaact cctcctccat cgagatcatc ggcgtgccgc cggaggggcg cgcgggcac    960
ggctacatca cctcggcga ctacctcgtg tacaagtcca tcgacttcgg caacggcgcc   1020
acctccttca aggccaaggt ggccaacgcc aacacctcca acatcgagct tcgcctcaac   1080
ggcccgaacg gcacctcat cggcaccctc tcggtgaagt ccaccggcga ctggaacacc   1140
tacgaggagc agacctgctc catctccaag gtgaaccggc tcaacgacct ctacctcgtg   1200
ttcaagggcc cggtgaaatc cgactgggtc accttcggcg tgtccgagaa ggacgaactc   1260
tag                                                                    1263

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<210> 108
 <211> 420
 <212> PRT
 <213> artificial sequence

<220>
 <223> plasmid 13347

<400> 108

```

Met Arg Val Leu Leu Val Ala Leu Ala Leu Leu Ala Leu Ala Ala Ser
1           5           10           15

```

```

Ala Thr Ser Met Ala Ala Ser Leu Pro Thr Met Pro Pro Ser Gly Tyr
20           25           30

```

```

Asp Gln Val Arg Asn Gly Val Pro Arg Gly Gln Val Val Asn Ile Ser
35           40           45

```

```

Tyr Phe Ser Thr Ala Thr Asn Ser Thr Arg Pro Ala Arg Val Tyr Leu
50           55           60

```

```

Pro Pro Gly Tyr Ser Lys Asp Lys Lys Tyr Ser Val Leu Tyr Leu Leu
65           70           75           80

```

His Gly Ile Gly Gly Ser Glu Asn Asp Trp Phe Glu Gly Gly Gly Arg
 85 90 95

Ala Asn Val Ile Ala Asp Asn Leu Ile Ala Glu Gly Lys Ile Lys Pro
 100 105 110

Leu Ile Ile Val Thr Pro Asn Thr Asn Ala Ala Gly Pro Gly Ile Ala
 115 120 125

Asp Gly Tyr Glu Asn Phe Thr Lys Asp Leu Leu Asn Ser Leu Ile Pro
 130 135 140

Tyr Ile Glu Ser Asn Tyr Ser Val Tyr Thr Asp Arg Glu His Arg Ala
 145 150 155 160

Ile Ala Gly Leu Ser Met Gly Gly Gly Gln Ser Phe Asn Ile Gly Leu
 165 170 175

Thr Asn Leu Asp Lys Phe Ala Tyr Ile Gly Pro Ile Ser Ala Ala Pro
 180 185 190

Asn Thr Tyr Pro Asn Glu Arg Leu Phe Pro Asp Gly Gly Lys Ala Ala
 195 200 205

Arg Glu Lys Leu Lys Leu Leu Phe Ile Ala Cys Gly Thr Asn Asp Ser
 210 215 220

Leu Ile Gly Phe Gly Gln Arg Val His Glu Tyr Cys Val Ala Asn Asn
 225 230 235 240

Ile Asn His Val Tyr Trp Leu Ile Gln Gly Gly Gly His Asp Phe Asn
 245 250 255

Val Trp Lys Pro Gly Leu Trp Asn Phe Leu Gln Met Ala Asp Glu Ala
 260 265 270

Gly Leu Thr Arg Asp Gly Asn Thr Pro Val Pro Thr Pro Ser Pro Lys
 275 280 285

Pro Ala Asn Thr Arg Ile Glu Ala Glu Asp Tyr Asp Gly Ile Asn Ser
 290 295 300

Ser Ser Ile Glu Ile Ile Gly Val Pro Pro Glu Gly Gly Arg Gly Ile
305 310 315 320

Gly Tyr Ile Thr Ser Gly Asp Tyr Leu Val Tyr Lys Ser Ile Asp Phe
325 330 335

Gly Asn Gly Ala Thr Ser Phe Lys Ala Lys Val Ala Asn Ala Asn Thr
340 345 350

Ser Asn Ile Glu Leu Arg Leu Asn Gly Pro Asn Gly Thr Leu Ile Gly
355 360 365

Thr Leu Ser Val Lys Ser Thr Gly Asp Trp Asn Thr Tyr Glu Glu Gln
370 375 380

Thr Cys Ser Ile Ser Lys Val Thr Gly Ile Asn Asp Leu Tyr Leu Val
385 390 395 400

Phe Lys Gly Pro Val Asn Ile Asp Trp Phe Thr Phe Gly Val Ser Glu
405 410 415

Lys Asp Glu Leu
420

<210> 109
<211> 1296
<212> DNA
<213> artificial sequence

<220>
<223> plasmid 11267

<400> 109
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gcgcagtcgc agccggagct gaagctggag tccgtggtga tcgtgtcccg ccacggcgctg 120
cgcgccccga ccaaggccac ccagctcatg caggacgtga ccccggaacgc ctggccgacc 180
tggccggtga agctcggcga gctgaccccg cgcggcggcg agctgatcgc ctacctcggc 240
cactactggc gccagcgccct cgtggccgac ggccctctcc cgaagtgcgg ctgcccgcag 300
tccggccagg tggccatcat cgcgcagctg gacgagcgca cccgcaagac cggcgaggcc 360
ttcgccgcgc gcctcgcccc ggactgcgcc atcaccgtgc acaccaggc cgacacctcc 420
tccccggacc cgctcttcaa cccgctcaag accggcggtgt gccagctcga caacgccaac 480
gtgaccgacg ccatactgga gcgcgcgggc ggctccatcg ccgacttcac cggccactac 540

```

cagaccgcct tccgcgagct ggagcgcgtg ctcaacttcc cgcagtccaa cctctgcctc      600
aagcgcgaga agcaggacga gtcctgctcc ctcacccagg ccctcccgtc cgagctgaag      660
gtgtccgcgc actgcgtgtc cctcaccggc gccgtgtccc tcgcctccat gctcaccgaa      720
atcttctctcc tccagcaggc ccagggcatg ccggagccgg gctggggccg catcaccgac      780
tcccaccagt ggaacacctt cctctccctc cacaacgccc agttcgacct cctccagcgc      840
accccgaggg tggcccgtc cgcgcgcacc ccgtctctcg acctcatcaa gaccgcctc      900
accccgaccc cgcgcgagaa gcaggcctac ggcgtgaccc tcccacctc cgtgctcttc      960
atcgccggcc acgacaccaa cctcgccaac ctcggcggcg ccctggagct gaactggacc     1020
ctcccgggcc agccggacaa cccccgcgcg ggcggcgagc tgggtgttcga gcgctggcgc     1080
cgctctctcg acaactccca gtggattcag gtgtccctcg tgttcagac cctccagcag     1140
atgcgcgaca agaccccgct ctccctcaac acccgcgcgg gcgaggtgaa gctcacctc     1200
gccggctgcg aggagcgcaa cgcgcagggc atgtgctccc tcgccggctt caccagatc     1260
gtgaacgagg cccgcctccc ggctgctcc ctctaa                                1296

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<210> 110

<211> 431

<212> PRT

<213> artificial sequence

<220>

<223> plasmid 11267 aa sequence

<400> 110

```

Met Arg Val Leu Leu Val Ala Leu Ala Leu Leu Ala Leu Ala Ala Ser
1           5           10           15

```

```

Ala Thr Ser Ala Ala Gln Ser Glu Pro Glu Leu Lys Leu Glu Ser Val
20           25           30

```

```

Val Ile Val Ser Arg His Gly Val Arg Ala Pro Thr Lys Ala Thr Gln
35           40           45

```

```

Leu Met Gln Asp Val Thr Pro Asp Ala Trp Pro Thr Trp Pro Val Lys
50           55           60

```

```

Leu Gly Glu Leu Thr Pro Arg Gly Gly Glu Leu Ile Ala Tyr Leu Gly
65           70           75           80

```

His Tyr Trp Arg Gln Arg Leu Val Ala Asp Gly Leu Leu Pro Lys Cys
 85 90 95

Gly Cys Pro Gln Ser Gly Gln Val Ala Ile Ile Ala Asp Val Asp Glu
 100 105 110

Arg Thr Arg Lys Thr Gly Glu Ala Phe Ala Ala Gly Leu Ala Pro Asp
 115 120 125

Cys Ala Ile Thr Val His Thr Gln Ala Asp Thr Ser Ser Pro Asp Pro
 130 135 140

Leu Phe Asn Pro Leu Lys Thr Gly Val Cys Gln Leu Asp Asn Ala Asn
 145 150 155 160

Val Thr Asp Ala Ile Leu Glu Arg Ala Gly Gly Ser Ile Ala Asp Phe
 165 170 175

Thr Gly His Tyr Gln Thr Ala Phe Arg Glu Leu Glu Arg Val Leu Asn
 180 185 190

Phe Pro Gln Ser Asn Leu Cys Leu Lys Arg Glu Lys Gln Asp Glu Ser
 195 200 205

Cys Ser Leu Thr Gln Ala Leu Pro Ser Glu Leu Lys Val Ser Ala Asp
 210 215 220

Cys Val Ser Leu Thr Gly Ala Val Ser Leu Ala Ser Met Leu Thr Glu
 225 230 235 240

Ile Phe Leu Leu Gln Gln Ala Gln Gly Met Pro Glu Pro Gly Trp Gly
 245 250 255

Arg Ile Thr Asp Ser His Gln Trp Asn Thr Leu Leu Ser Leu His Asn
 260 265 270

Ala Gln Phe Asp Leu Leu Gln Arg Thr Pro Glu Val Ala Arg Ser Arg
 275 280 285

Ala Thr Pro Leu Leu Asp Leu Ile Lys Thr Ala Leu Thr Pro His Pro
 290 295 300

Pro Gln Lys Gln Ala Tyr Gly Val Thr Leu Pro Thr Ser Val Leu Phe
 305 310 315 320

Ile Ala Gly His Asp Thr Asn Leu Ala Asn Leu Gly Gly Ala Leu Glu
 325 330 335

Leu Asn Trp Thr Leu Pro Gly Gln Pro Asp Asn Thr Pro Pro Gly Gly
 340 345 350

Glu Leu Val Phe Glu Arg Trp Arg Arg Leu Ser Asp Asn Ser Gln Trp
 355 360 365

Ile Gln Val Ser Leu Val Phe Gln Thr Leu Gln Gln Met Arg Asp Lys
 370 375 380

Thr Pro Leu Ser Leu Asn Thr Pro Pro Gly Glu Val Lys Leu Thr Leu
 385 390 395 400

Ala Gly Cys Glu Glu Arg Asn Ala Gln Gly Met Cys Ser Leu Ala Gly
 405 410 415

Phe Thr Gln Ile Val Asn Glu Ala Arg Ile Pro Ala Cys Ser Leu
 420 425 430

<210> 111
 <211> 1314
 <212> DNA
 <213> artificial sequence

<220>
 <223> plasmid 11268

<400> 111
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 cgcgccccga ccaaggccac ccagctcatg caggacgtga ccccgacgc ctggccgacc 180
 tggccggtga agctcggcga gctgaccccg cgcggcggcg agctgatcgc ctacctcggc 240
 cactactggc gccagcgct cgtggccgac ggctcctcc cgaagtgcgg ctgcccgag 300
 tccggccagg tggccatcat cgcgcagctg gacgagcgca cccgcaagac cggcgaggcc 360
 ttgcgcgcg gcctcgcccc ggactgcgac atcacgtgc acaccaggc cgacacctcc 420
 tccccggacc cgctcttcaa cccgctcaag accggcggtg gccagctcga caacgccaac 480
 gtgaccgacg ccatactgga gcgcgcggc ggctccatcg ccgacttcac cggccactac 540
 cagaccgcct tcgcgagct ggagcgcgtg ctcaacttcc cgcagtccaa cctctgcctc 600

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aagcgcgaga agcaggacga gtctgtctcc ctaccccagg ccctcccgtc cgagctgaag      660
gtgtccgccc actgctgttc cctcaccggc gccgtgtccc tcgcctccat gctcaccgaa      720
atcttctctc tccagcaggc ccagggcatg ccggagccgg gctggggccg catcaccgac      780
tcccaccagt ggaacaccct cctctccctc cacaacgccc agttcgacct cctccagcgc      840
accccgaggg tggcccgcct ccgcgccacc ccgctcctcg acctcatcaa gaccgccctc      900
accccgaccc cgccgcagaa gcaggcctac ggcgtgaccc tcccgaacct cgtgctcttc      960
atcgccggcc acgacaccaa cctcgccaac ctcggcggcg ccctggagct gaactggacc     1020
ctcccggggc agccggacaa cccccgcgg ggcggcgagc tgggtgttcga gcgctggcgc     1080
cgctctctcc acaactccca gtggattcag gtgtccctcg tgttccagac cctccagcag     1140
atgcgcgaca agaccccgct ctccctcaac accccgcggg gcgaggtgaa gctcaccctc     1200
gccggctgcg aggagcgcaa cgccagggc atgtgtctcc tcgcgggctt caccagatc      1260
gtgaacgagg cccgcatccc ggcctgtctc ctctccgaga aggacgagct gtaa          1314

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<210> 112

<211> 437

<212> PRT

<213> artificial sequence

<220>

<223> plasmid 11268 amino acid sequence

<400> 112

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Met Arg Val Leu Leu Val Ala Leu Ala Leu Leu Ala Leu Ala Ala Ser
1           5           10          15

```

```

Ala Thr Ser Ala Ala Gln Ser Glu Pro Glu Leu Lys Leu Glu Ser Val
20          25          30

```

```

Val Ile Val Ser Arg His Gly Val Arg Ala Pro Thr Lys Ala Thr Gln
35          40          45

```

```

Leu Met Gln Asp Val Thr Pro Asp Ala Trp Pro Thr Trp Pro Val Lys
50          55          60

```

```

Leu Gly Glu Leu Thr Pro Arg Gly Gly Glu Leu Ile Ala Tyr Leu Gly
65          70          75          80

```

```

His Tyr Trp Arg Gln Arg Leu Val Ala Asp Gly Leu Leu Pro Lys Cys
85          90          95

```

Gly Cys Pro Gln Ser Gly Gln Val Ala Ile Ile Ala Asp Val Asp Glu
 100 105 110
 Arg Thr Arg Lys Thr Gly Glu Ala Phe Ala Ala Gly Leu Ala Pro Asp
 115 120 125
 Cys Ala Ile Thr Val His Thr Gln Ala Asp Thr Ser Ser Pro Asp Pro
 130 135 140
 Leu Phe Asn Pro Leu Lys Thr Gly Val Cys Gln Leu Asp Asn Ala Asn
 145 150 155 160
 Val Thr Asp Ala Ile Leu Glu Arg Ala Gly Gly Ser Ile Ala Asp Phe
 165 170 175
 Thr Gly His Tyr Gln Thr Ala Phe Arg Glu Leu Glu Arg Val Leu Asn
 180 185 190
 Phe Pro Gln Ser Asn Leu Cys Leu Lys Arg Glu Lys Gln Asp Glu Ser
 195 200 205
 Cys Ser Leu Thr Gln Ala Leu Pro Ser Glu Leu Lys Val Ser Ala Asp
 210 215 220
 Cys Val Ser Leu Thr Gly Ala Val Ser Leu Ala Ser Met Leu Thr Glu
 225 230 235 240
 Ile Phe Leu Leu Gln Gln Ala Gln Gly Met Pro Glu Pro Gly Trp Gly
 245 250 255
 Arg Ile Thr Asp Ser His Gln Trp Asn Thr Leu Leu Ser Leu His Asn
 260 265 270
 Ala Gln Phe Asp Leu Leu Gln Arg Thr Pro Glu Val Ala Arg Ser Arg
 275 280 285
 Ala Thr Pro Leu Leu Asp Leu Ile Lys Thr Ala Leu Thr Pro His Pro
 290 295 300
 Pro Gln Lys Gln Ala Tyr Gly Val Thr Leu Pro Thr Ser Val Leu Phe
 305 310 315 320

Ile Ala Gly His Asp Thr Asn Leu Ala Asn Leu Gly Gly Ala Leu Glu
325 330 335

Leu Asn Trp Thr Leu Pro Gly Gln Pro Asp Asn Thr Pro Pro Gly Gly
340 345 350

Glu Leu Val Phe Glu Arg Trp Arg Arg Leu Ser Asp Asn Ser Gln Trp
355 360 365

Ile Gln Val Ser Leu Val Phe Gln Thr Leu Gln Gln Met Arg Asp Lys
370 375 380

Thr Pro Leu Ser Leu Asn Thr Pro Pro Gly Glu Val Lys Leu Thr Leu
385 390 395 400

Ala Gly Cys Glu Glu Arg Asn Ala Gln Gly Met Cys Ser Leu Ala Gly
405 410 415

Phe Thr Gln Ile Val Asn Glu Ala Arg Ile Pro Ala Cys Ser Leu Ser
420 425 430

Glu Lys Asp Glu Leu
435